

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 17, 2006, 01:25:09 ; Search time 47 Seconds  
(without alignments)  
561.139 Million cell updates/sec

Title: US-10-634-027-7

Perfect score: 1744  
Sequence: 1 GRPLSVHNLQKGNKRTS.....VDVLRARLKRSRHHHHH 319

Scoring table: BLOSUM62  
Gapop 10.0 ; Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/aa/5/COMB.pep:\*  
2: /cgn2\_6/prodata/1/aa/6/COMB.pep:\*  
3: /cgn2\_6/prodata/1/aa/H/COMB.pep:\*  
4: /cgn2\_6/prodata/1/aa/PCTUS/COMB.pep:\*  
5: /cgn2\_6/prodata/1/aa/R/COMB.pep:\*  
6: /cgn2\_6/prodata/1/aa/backfill1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1691	97.0	1997	2	US-09-949-016-6275 Sequence 6275, Ap
2	1644	94.3	1907	2	US-09-949-016-8045 Sequence 8045, Ap
3	1444	82.8	278	1	US-08-201-697-16 Sequence 16, Appl
4	1374	78.8	254	1	US-08-685-925-14 Sequence 14, Appl
5	1374	78.8	254	1	US-09-144-925-14 Sequence 2, Appl1
6	878.5	50.4	1337	2	US-08-854-585-2 Sequence 2, Appl1
7	878.5	50.4	1337	2	US-09-447-533-2 Sequence 2, Appl1
8	878.5	50.4	1337	4	PCT-US95-05512-2 Sequence 17, Appl
9	843.5	48.4	273	1	US-08-201-697-17 Sequence 17, Appl
10	765	43.9	506	2	US-09-949-016-8833 Sequence 8833, Ap
11	765	43.9	506	2	US-09-949-016-8834 Sequence 8834, Ap
12	765	43.9	506	2	US-09-949-016-8835 Sequence 8835, Ap
13	765	43.9	506	2	US-09-949-016-8836 Sequence 8836, Ap
14	765	43.9	506	2	US-09-949-016-8837 Sequence 8837, Ap
15	765	43.9	506	2	US-09-949-016-8838 Sequence 8838, Ap
16	765	43.9	1274	2	US-09-949-016-8828 Sequence 8828, Ap
17	765	43.9	1274	2	US-09-949-016-8829 Sequence 8829, Ap
18	765	43.9	1274	2	US-09-949-016-8830 Sequence 8830, Ap
19	765	43.9	1274	2	US-09-949-016-8831 Sequence 8831, Ap
20	765	43.9	1274	2	US-09-949-016-8832 Sequence 8832, Ap
21	761.5	43.7	1188	1	US-08-201-697-4 Sequence 4, Appl
22	761.5	43.7	1246	2	US-09-949-016-8051 Sequence 8051, Ap
23	761.5	43.7	1246	2	US-09-949-016-8052 Sequence 8052, Ap
24	761.5	43.7	1246	2	US-09-949-016-8053 Sequence 8053, Ap
25	761.5	43.7	1246	2	US-09-949-016-8054 Sequence 8054, Ap
26	761.5	43.7	1246	2	US-09-949-016-8055 Sequence 8055, Ap
27	760.5	43.6	1187	1	US-08-201-697-2 Sequence 2, Appl1

28	744.5	42.7	251	1	US-08-685-992-15	Sequence 15, Appl
29	744.5	42.7	251	1	US-09-144-925-15	Sequence 15, Appl
30	697.5	40.0	1711	1	US-08-342-930-2	Sequence 2, Appl1
31	675	38.7	2301	2	US-08-822-871-4	Sequence 4, Appl
32	673	38.6	402	2	US-09-361-096A-15	Sequence 15, Appl
33	673	38.6	402	1	US-08-036-210-15	Sequence 15, Appl
34	673	38.6	402	1	US-08-449-609-15	Sequence 15, Appl
35	673	38.6	898	1	US-08-036-210-22	Sequence 22, Appl
36	673	38.6	898	1	US-08-449-609-22	Sequence 22, Appl
37	673	38.6	898	1	US-09-361-096A-22	Sequence 22, Appl
38	667	38.2	289	2	US-09-361-096A-47	Sequence 47, Appl
39	667	38.2	322	1	US-08-036-210-11	Sequence 11, Appl
40	667	38.2	322	1	US-08-449-609-11	Sequence 11, Appl
41	667	38.2	322	2	US-09-361-096A-11	Sequence 11, Appl
42	658	37.7	2291	2	US-09-822-871-2	Sequence 2, Appl
43	643.5	36.9	255	1	US-08-685-992-16	Sequence 16, Appl
44	643.5	36.9	255	1	US-09-144-925-16	Sequence 16, Appl
45	618.5	35.5	2314	2	US-09-816-703A-2	Sequence 2, Appl1

#### ALIGNMENTS

RESULT 1	US-09-949-016-6275	Sequence 6275, Application US/09949016
Patent No. 6812339		
GENERAL INFORMATION:		
APPLICANT: VENTUR, J. Craig et al.		
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASES, METHODS OF DETECTION AND USES THEREOF		
FILE REFERENCE: CL001037		
CURRENT APPLICATION NUMBER: US/09/949, 016		
PRIOR FILING DATE: 2000-04-14		
PRIOR APPLICATION NUMBER: 60/241,755		
PRIOR FILING DATE: 2000-10-20		
PRIOR APPLICATION NUMBER: 60/237,768		
PRIOR FILING DATE: 2000-10-03		
PRIOR APPLICATION NUMBER: 60/231,498		
PRIOR FILING DATE: 2000-09-08		
NUMBER OF SEQ ID NOS: 207012		
SOFTWARE: FASTSEQ for Windows Version 4.0		
SEQ ID NO 6275		
LENGTH: 1997		
TYPE: PRT		
ORGANISM: Human		
US-09-949-016-6275		
Query Match	97.0%	Score 1691; DB 2; Length 1997;
Best Local Similarity	99.4%	Pred. No 8.1e-170;
Matches 312; Conservative 1; Mismatches 1; Indels 0; Gaps 0;		
QY	2	DRLSVHNLQKGNKRTSCPTKINQFBGFMKLDNSYILSKYEBELKVGKRGSCDI 61
DB	1662	DRLSVHNLQKGNKRTSCPTKINQFBGFMKLDNSYILSKYEBELKVGKRGSCDI 1721
QY	62	ALLPENGKNNYNNILPYDATVVKLSVDDPCSDYINASYIPNNFREYVLTGGLPG 121
DB	1722	ALLPENGKNNYNNILPYDATVVKLSVDDPCSDYINASYIPNNFREYVLTGGLPG 1781
QY	122	TKDDFWKMWQNNYNNIVWVTCVEKRVKCHWYPADODSLYYGDLILQMLSESVLEW 181
DB	1782	TKDDFWKMWQNNYNNIVWVTCVEKRVKCHWYPADODSLYYGDLILQMLSESVLEW 1841
QY	182	TIREPKTGESEDLARHLIRHFTYVWPDHGVETTSOLIOFYRVTRDYINNSPCAGPTV 241
DB	1842	TIREPKTGESEDLARHLIRHFTYVWPDHGVETTSOLIOFYRVTRDYINNSPCAGPTV 1901
QY	242	VHCSAGVGRGTFTALDRILQDLSKDSVDIYGAVHDLRLRWVMTGECOVVYHGCVR 301
DB	1902	VHCSAGVGRGTFTALDRILQDLSKDSVDIYGAVHDLRLRWVMTGECOVVYHGCVR 1961
QY	302	DVLARKLRSEQH 315

Db 1962 DVLARKLSEBOEN 1975

## RESULT 2

US-09-949-016-8049  
Sequence 8049, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

FILE REFERENCE: C1001307

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20, 755

PRIOR FILING DATE: 2000-10-20, 768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 8049

LENGTH: 1903

TYPE: PRT

ORGANISM: Human

US-09-949-016-8049

Query Match 94.3%; Score 1644; DB 2; Length 1903;  
Best Local Similarity 97.5%; Pred. No. 7,4e-165;

Matches 306; Conservative 1; Mismatches 1; Indels 6; Gaps 1;

Db 1574 DRPLSHMLGKGRKTSQPKINQFEGHFMKLDADSNYLSKEYEELKDVGRNOSCDI 61  
1574 DRPLSHMLGKGRKTSQPKINQFEGHFMKLDADSNYLSKEYEELKDVGRNOSCDI 1627

Qy 62 ALPBRGKRNILPYDAPATRYKLSNDPPSCSDYINASYRGNRRRYTYTGCPPLG 121  
1628 ALPBRGKRNILPYDAPATRYKLSNDPPSCSDYINASYRGNRRRYTYTGCPPLG 1687

Qy 122 TKODFWKWEONVNIYVNTQCEKGRKCDHWAPADDSLYTGDLILQMLSEVLEW 181  
1688 TKODFWKWEONVNIYVNTQCEKGRKCDHWAPADDSLYTGDLILQMLSEVLEW 1747

Qy 182 TIREFKICEBOLDARHLRHFHYTWPDPHGVPTTOSLIQFRTVADYINRSPAGPTV 241  
1748 TIREFKICEBOLDARHLRHFHYTWPDPHGVPTTOSLIQFRTVADYINRSPAGPTV 1807

Qy 242 VHSAGVGTGTFTALDRILQQLDSKDSVDIYGAVHDLRLHRVHMVQTECOYVYLHQCVR 301  
1808 VHSAGVGTGTFTALDRILQQLDSKDSVDIYGAVHDLRLHRVHMVQTECOYVYLHQCVR 1867

Qy 302 DVLARKLSEBOEN 1881  
1868 DVLARKLSEBOEN 1881

Db 1868 DVLARKLSEBOEN 1881

RESULT 3  
US-08-201-697-16  
Sequence 16, Application US/08201697

Patent No. 5705823

GENERAL INFORMATION:

APPLICANT: Miggins, Roger C.

APPLICANT: Thomas, Feedikayil E.

TITLE OF INVENTION: Mammalian Glomerular Epithelial Protein

TITLE OF INVENTION: 1

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell and Flores

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/201,697

FILING DATE: 25-FEB-1994

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-UM 9783

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 278 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-201-697-16

Query Match 82.8%; Score 1444; DB 1; Length 278;  
Best Local Similarity 95.7%; Pred. No. 6,9e-145;

Matches 266; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 22 PIKINQFEGHFMKLDADSNYLSKEYEELKDVGRNOSCDIALLPENRGRKRNINILPYDA 81  
Db 1 PIKINQFEGHFMKLDADSNYLSKEYEELKDVGRNOSCDIALLPENRGRKRNINILPYDA 60

Qy 82 TVKLKSNVDDPCSDYINASYRGNRRRYTYTGCPPLG 141  
Db 61 TVKLKSNVDDPCSDYINASYRGNRRRYTYTGCPPLG 120

Qy 142 TQCEKGRKCDHWAPADDSLYTGDLILQMLSEVLEW 201  
Db 121 TQCEKGRKCDHWAPADDSLYTGDLILQMLSEVLEW 180

Qy 202 NHTTWPDPHGVPTTOSLIQFRTVADYINRSPAGPTV 261  
Db 181 NHTTWPDPHGVPTTOSLIQFRTVADYINRSPAGPTV 240

Qy 262 QQLDSKDSVDIYGAVHDLRLHRVHMVQTECOYVYLHQCVR 299  
Db 241 QQLDSKDSVDIYGAVHDLRLHRVHMVQTECOYVYLHQCVR 278

RESULT 4  
US-08-685-992-14  
Sequence 14, Application US/08685992

Patent No. 5912138

GENERAL INFORMATION:

APPLICANT: Tonks, Nicholas

APPLICANT: Flint, Andrew J.

TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN

TITLE OF INVENTION: TYROSINE PHOSPHATASES

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: HANITON, BROOK, SMITH & REYNOLDS, P.C.

STREET: Two Millitia Drive

CITY: Lexington

STATE: MA

COUNTRY: USA

ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: FASTSEQ for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/685,992  
FILING DATE: 25-JUL-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: CSHL96-03  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 781-861-6240  
TELEFAX: 781-861-9540  
TELEX:  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 254 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-685-992-14

Query Match 78.8%; Score 1374; DB 1; Length 254;  
Best Local Similarity 99.2%; Pred. No. 1,6e-137;  
Matches 254; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 56 NOSCDIALPENRNGKRRNNILPYDARVYLSNVDDPCSDYINASYIPGNVFRREYIVT 115  
DB 1 NOSCDIALPENRNGKRRNNILPYDARVYLSNVDDPCSDYINASYIPGNVFRREYIVT 60  
QY 116 QGRLPTGDDPMKWMQWVNIWVTCVEKGRVYCDHWAPADQSLYGGDLILQMLSE 175  
DB 61 QGRLPTGDDPMKWMQWVNIWVTCVEKGRVYCDHWAPADQSLYGGDLILQMLSE 120  
QY 176 SVLEPMTREFKICGEEQLDAHRLIRHFIYTWPDHGVPEFTOSLIQFRTVRYINRSP 235  
DB 121 SVLEPMT--FKICGEEQLDAHRLIRHFIYTWPDHGVPEFTOSLIQFRTVRYINRSP 178  
QY 236 GAGPTVWCSAGVGRGTFTIALDRILQQLDSKDSVDIYGAHDLRLHRYHVMVQTECOYV 295  
DB 179 GAGPTVWCSAGVGRGTFTIALDRILQQLDSKDSVDIYGAHDLRLHRYHVMVQTECOYV 238  
QY 296 LHQCVRDVLRARKLRS 311  
DB 239 LHQCVRDVLRARKLRS 254

RESULT 5  
US-09-144-925-14  
Sequence 14, Application US/09144925  
Patent No. 5951979  
GENERAL INFORMATION:  
APPLICANT: Tonks, Nicholas  
APPLICANT: Flint, Andrew J.  
TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN  
TITLE OF INVENTION: TYROSINE PHOSPHATASES  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.  
STREET: TWO MILITIA DRIVE  
CITY: Lexington  
STATE: MA  
COUNTRY: USA  
ZIP: 02421-4799  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: FASTSEQ for Windows version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/144,925  
FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/685,992  
FILING DATE: July 25, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: CSHL96-03Z  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 781-861-6240  
TELEFAX: 781-861-9540  
TELEX:  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 254 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-144-925-14

Query Match 78.8%; Score 1374; DB 1; Length 254;  
Best Local Similarity 99.2%; Pred. No. 1,6e-137;  
Matches 254; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 56 NOSCDIALPENRNGKRRNNILPYDARVYLSNVDDPCSDYINASYIPGNVFRREYIVT 115  
DB 1 NOSCDIALPENRNGKRRNNILPYDARVYLSNVDDPCSDYINASYIPGNVFRREYIVT 60  
QY 116 QGRLPTGDDPMKWMQWVNIWVTCVEKGRVYCDHWAPADQSLYGGDLILQMLSE 175  
DB 61 QGRLPTGDDPMKWMQWVNIWVTCVEKGRVYCDHWAPADQSLYGGDLILQMLSE 120  
QY 176 SVLEPMTREFKICGEEQLDAHRLIRHFIYTWPDHGVPEFTOSLIQFRTVRYINRSP 235  
DB 121 SVLEPMT--FKICGEEQLDAHRLIRHFIYTWPDHGVPEFTOSLIQFRTVRYINRSP 178  
QY 236 GAGPTVWCSAGVGRGTFTIALDRILQQLDSKDSVDIYGAHDLRLHRYHVMVQTECOYV 295  
DB 179 GAGPTVWCSAGVGRGTFTIALDRILQQLDSKDSVDIYGAHDLRLHRYHVMVQTECOYV 238  
QY 296 LHQCVRDVLRARKLRS 311  
DB 239 LHQCVRDVLRARKLRS 254

RESULT 6  
US-08-854-585-2  
Sequence 2, Application US/08854585  
Patent No. 6114140  
GENERAL INFORMATION:  
APPLICANT: Tonks, Nicholas K. and Stefan, Arne  
TITLE OF INVENTION: Density Enhanced Protein Tyrosine Phosphatase  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 233 South Wacker Drive, Suite 6300  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/854,585  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/237,940  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:

NAME: Borun, Michael F.  
 REGISTRATION NUMBER: 25,447  
 REFERENCE/DOCKET NUMBER: 27866/11954  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312-474-6300  
 TELEFAX: 312-474-0448  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1337 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-854-585-2

Query Match 50.4%; Score 878.5; DB 2; Length 1337;  
 Best Local Similarity 56.4%; Pred. No. 98-84;  
 Matches 164; Conservative 56; Mismatches 68; Indels 3; Gaps 3;

18 KTSCPIKINOFESGFMKLDADSNLSSKEIEKDVGRNOSCDIALLEPNRGKRRNNTL 77  
 1016 KKSRLIRVENFEAYFKQADSNCGFAEYEDLKVGISOPKYAELEENRGKRRNNTL 1075  
 78 PDATRVYLSNVDDPCSDYINASYIPGNFRREYIVTQGPLPGTKDDFWRMWMEQNVHN 137  
 1076 PDISRVLKLS-VQTHSTDDYINAWMPGYHSKDFIATQGPLPNTLKDPMRMWMEQNVYA 1134  
 138 IYMTQCEKGRVKCDHWPADQPSLYGDLILQMLSESVLPMTIRREFKICEBOLDNAH 197  
 1135 IIMLKCEGGRKCEBYWPSKQ-ADYGDIVAMTSEIVLPMTIRDFTVKNIQTSSEH 1193  
 198 RLIRFHYTWPHGVPETQSILQFVTVRDYINRSPGAPTVVHCSAGVGRGTFFIAL 257  
 1194 PL-RQFHTSMPHGVPDTDLINFRILVRDMKQSPSPSPILVHCAGVGRGTFFIAL 1252  
 258 DRILOQSDSDSYDIYGAHDLRLHVRHNVQTEQYVYLHQCVRDYLAARK 308  
 1253 DRLIYQENNVYDYGIVYDLRHRPLMVQTEQYVFLNQCVDIVASQK 1303

RESULT 7  
 US-09-447-533-2  
 Sequence 2, Application US/09447533  
 Patent No. 6552169  
 GENERAL INFORMATION:  
 APPLICANT: Tonks, Nicholas K.  
 Oelman, Arne  
 TITLE OF INVENTION: DENSITY ENHANCED PROTEIN TYROSINE  
 PHOSPHATASES  
 NUMBER OF SEQUENCES: 6  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Seed IP Law Group PLLC  
 STREET: Suite 6300, 701 Fifth Avenue  
 CITY: Seattle  
 STATE: Washington  
 COUNTRY: USA  
 ZIP: 98104  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/447,533  
 FILING DATE: 23-NOV-95  
 CLASSIFICATION: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Rosenman Ph.D., Stephen J.  
 REGISTRATION NUMBER: 43,058  
 REFERENCE/DOCKET NUMBER: 200125, 402C1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (206) 622-4900  
 TELEFAX: (206) 682-6031  
 INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 1337 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 US-09-447-533-2

Query Match 50.4%; Score 878.5; DB 2; Length 1337;  
 Best Local Similarity 56.4%; Pred. No. 98-84;  
 Matches 164; Conservative 56; Mismatches 68; Indels 3; Gaps 3;

18 KTSCPIKINOFESGFMKLDADSNLSSKEIEKDVGRNOSCDIALLEPNRGKRRNNTL 77  
 1016 KKSRLIRVENFEAYFKQADSNCGFAEYEDLKVGISOPKYAELEENRGKRRNNTL 1075  
 78 PDATRVYLSNVDDPCSDYINASYIPGNFRREYIVTQGPLPGTKDDFWRMWMEQNVHN 137  
 1076 PDISRVLKLS-VQTHSTDDYINAWMPGYHSKDFIATQGPLPNTLKDPMRMWMEQNVYA 1134  
 138 IYMTQCEKGRVKCDHWPADQPSLYGDLILQMLSESVLPMTIRREFKICEBOLDNAH 197  
 1135 IIMLKCEGGRKCEBYWPSKQ-ADYGDIVAMTSEIVLPMTIRDFTVKNIQTSSEH 1193  
 198 RLIRFHYTWPHGVPETQSILQFVTVRDYINRSPGAPTVVHCSAGVGRGTFFIAL 257  
 1194 PL-RQFHTSMPHGVPDTDLINFRILVRDMKQSPSPSPILVHCAGVGRGTFFIAL 1252  
 258 DRILOQSDSDSYDIYGAHDLRLHVRHNVQTEQYVYLHQCVRDYLAARK 308  
 1253 DRLIYQENNVYDYGIVYDLRHRPLMVQTEQYVFLNQCVDIVASQK 1303

RESULT 8  
 PCT-US95-05512-2  
 Sequence 2, Application PC/TUS9505512  
 GENERAL INFORMATION:  
 APPLICANT: Tonks, Nicholas K. and steman, Arne  
 TITLE OF INVENTION: Density Enhanced Protein Tyrosine  
 PHOSPHATASE  
 NUMBER OF SEQUENCES: 6  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Marshall, O'Toole, Garstein, Murray &  
 STREET: 233 South Wacker Drive, Suite 6300  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: United States of America  
 ZIP: 60606  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: IBM PC compatible  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US95/05512  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Borun, Michael F.  
 REGISTRATION NUMBER: 25,447  
 REFERENCE/DOCKET NUMBER: 27866/11954  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312-474-6300  
 TELEFAX: 312-474-0448  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1337 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 PCT-US95-05512-2  
 Query Match 50.4%; Score 878.5; DB 4; Length 1337;

Best Local Similarity 56.4%; Pred. No. 9e-84;  
Matches 164; Conservative 56; Mismatches 68; Indels 3; Gaps 3;

QY 18 KTSCKPKNQEGHFMKLDADSNYLSKYEELKDVGRNOSCDIALPERKGNKNNIL 77  
DB 1016 KSKRLRKNFPAFKQKQADSKCFABEYEDLKVISQPKYALAEKRGKNNIVL 1075  
QY 78 PYDATVYKLSNVDDPCSDYINASYIPGNRRBYIVTQGLPGTKODFMKRWMEQNNH 137  
DB 1076 PYDISRVKLS-VQTHSTDDYINANNYPMGYSHKQDFATQGLPPTLADFMKRWMEQNNH 1134  
QY 138 IYAVTQCEVKGKRVKCDHYWPAODSLVYGDILLQMLSESVLPEWTIREPKICGEOLDAH 197  
DB 1135 IYVLTQCEVKGKRVKCDHYWPAODSLVYGDILLQMLSESVLPEWTIREPKICGEOLDAH 1193  
QY 198 RLIRHRYTWPDHGVPEPTQSLIQFRTVADYINRSPAGPTVWCHSAGVGTGTPIAL 257  
DB 1194 PL-RQHFTSPDHGVPEPTQSLIQFRTVADYINRSPAGPTVWCHSAGVGTGTPIAL 1252  
QY 258 DRILQDSDYDIYGAVHDLRLHRYWVQTCQVYVHQCVDVLRARK 308  
DB 1253 DRILQDSDYDIYGAVHDLRLHRYWVQTCQVYVHQCVDVLRARK 1303

RESULT 9  
US-08-201-697-17  
Sequence 17, Application US/08201697  
Patent No. 5705623  
GENERAL INFORMATION:  
APPLICANT: Wiggins, Roger C.  
TITLE OF INVENTION: Mammalian Glomerular Epithelial Protein  
TITLE OF INVENTION: 1  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell and Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/201,697  
FILING DATE: 25-FEB-1994  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-UM 9783  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-8949  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 273 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-201-697-17

Query Match 48.4%; Score 843.5; DB 1; Length 273;  
Best Local Similarity 56.3%; Pred. No. 4.2e-81;  
Matches 157; Conservative 44; Mismatches 71; Indels 7; Gaps 3;

QY 22 PIKINQEGHFMKLDADSNYLSKYEELKDVGRNOSCDIALPERKGNKNNILPYDA 81  
DB 1 PIKINQEGHFMKLDADSNYLSKYEELKDVGRNOSCDIALPERKGNKNNILPYDA 60  
QY 82 TRVLSNVDDPCSDYINASYIPGNRRBYIVTQGLPGTKODFMKRWMEQNNHIVM 141

DB 61 SHFLQVDDSDSYINANNYVPGHNSPREFIVTQGLSTDDFMKRWMEQNNHIVM 120  
QY 142 TQCEKRVKCDHYWPAODSLVYGDILLQMLSESVLPEWTIREPKIC-GEOLDAHRI 200  
DB 121 TQCEKRVKCDHYWPAODSLVYGDILLQMLSESVLPEWTIREPKIC-GEOLDAHRI 176  
QY 201 RHFTVWPDHGVPEPTQSLIQFRTVADYINRSPAGPTVWCHSAGVGTGTPIALDI 260  
DB 177 RHFTVWPDHGVPEPTQSLIQFRTVADYINRSPAGPTVWCHSAGVGTGTPIALDI 234  
QY 261 LQDSDYDIYGAVHDLRLHRYWVQTCQVYVHQCVDVLRARK 299  
DB 235 LQDSDYDIYGAVHDLRLHRYWVQTCQVYVHQCVDVLRARK 110C

RESULT 10  
US-09-949-016-8833  
Sequence 8833, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: C1001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
PRIOR FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 8833  
LENGTH: 506  
TYPE: PRT  
ORGANISM: Human  
US-09-949-016-8833

Query Match 43.9%; Score 765; DB 2; Length 506;  
Best Local Similarity 48.2%; Pred. No. 2.3e-72;  
Matches 147; Conservative 59; Mismatches 89; Indels 10; Gaps 4;

QY 2 DRPLSVNLGQK--NRKTSCKPKNQEGHFMKLDADSNYLSKYEELKDVGRNOS 58  
DB 184 DYLAFLYINPMKNGKLRKLTWVQDDPDYIKMADSDYKFSQFEELKLTGLDIP 243  
QY 59 CDIALPERKGNKNNILPYDATVYKLSNVDDPCSDYINASYIPGNRRBYIVTQGLPG 118  
DB 244 HPAADLPKRCNKTNNILPYDSKVLVSNBEGADYINANNYPMGYSHKQDFATQGL 303  
QY 119 LPTKDDFMKRWMEQNNHIVTQGLQCEVKGKRVKCDHYWPAODSLVYGDILLQMLSES 176  
DB 304 LPTKDDFMKRWMEQNNHIVTQGLQCEVKGKRVKCDHYWPAODSLVYGDILLQMLSES 363  
QY 179 PEWTIREPKICGEOLDAHRLIRHRYWPDHGVPEPTQSLIQFRTVADYINRSPG 236  
DB 364 DWACRHFRI--NYADEMODVWHFNRYTWPDHGVPTANAAASIIQFVHNRQATKS-- 418  
QY 237 AGPTVWCHSAGVGTGTPIALDIQDSDYDIYGAVHDLRLHRYWVQTCQVYVHQC 296  
DB 419 KGPWTHCSAGVGTGTPIALDIQDSDYDIYGAVHDLRLHRYWVQTCQVYVHQC 234  
QY 297 HQCVR 301  
DB 479 HQCVQ 483

RESULT 11  
US-09-949-016-8834  
Sequence 8834, Application US/09949016

Patent No. 6812339  
 GENERAL INFORMATION:  
 APPLICANT: VENTER, J. Craig et al.  
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
 WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 FILE REFERENCE: C1001307  
 CURRENT APPLICATION NUMBER: US/09/949,016  
 CURRENT FILING DATE: 2000-04-14  
 PRIOR APPLICATION NUMBER: 60/241,755  
 PRIOR FILING DATE: 2000-10-20  
 PRIOR APPLICATION NUMBER: 60/237,768  
 PRIOR FILING DATE: 2000-10-03  
 PRIOR APPLICATION NUMBER: 60/231,498  
 PRIOR FILING DATE: 2000-09-08  
 NUMBER OF SEQ ID NOS: 207012  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 8834  
 LENGTH: 506  
 TYPE: PRT  
 ORGANISM: Human  
 US-09-949-016-8834

Query Match 43.9%; Score 765; DB 2; Length 506;  
 Best Local Similarity 48.2%; Pred. No. 2.3e-72;  
 Matches 147; Conservative 59; Mismatches 89; Indels 10; Gaps 4;

QY 2 DRPLSVHLNGGKG--NRKTSCKPIKNOFGHFMKLDNSNYLLSKEYEELKQVGRNOS 58  
 DB 184 DYLLAFYINPWSKNGKLGKRLTNVQLDDPDAIYKDWAKSDYKFSLOFEBELKIGLDIP 243  
 QY 59 CDIALPENRGKRRYNNILPYDATRYKLSNVDDPCSDYINASYIPGNFRREYIYTOGP 118  
 DB 244 HPAADLPANCKRRYNNILPYDSFRVLYSNMBEGADYINANYIPGNSPOEYIATQGP 303  
 QY 119 LPTGKDDPMKRWMEQNVNINVTQCVEKRGYKCDHWYPADDSLYGDDLQWLSSEVYL 178  
 DB 304 LPTKNDPMKRWVWVLOKSOIIVMLQCNKRRYKCDHWYPTPEPIAYGDIIVEMISEEQ 363  
 QY 179 PEWTIREFKICEBOLDHRLIRHFTYTWPDHGV--ETTSLOIOPRTYRDYINRSPG 236  
 DB 364 DDMACRHFRI--NYADMQDVHFTYTPADHGVPTANAAESILQFVHWVROQATKS-- 418  
 QY 237 AGPTVHCSAGVGTGTFIALDRILQQLDSKDSVDIYGAVHDLRLHRYHNVOTECQYVL 296  
 DB 419 KGPMTIHCSAGVGTGTFIALDRILQHIRDHFVDILGLVSEMRSTRMSVOTEBQYIFI 478  
 QY 297 HOCVR 301  
 DB 479 HOCVQ 483

RESULT 12  
 US-09-949-016-8835  
 Sequence 8835, Application US/09949016  
 Patent No. 6812339  
 GENERAL INFORMATION:  
 APPLICANT: VENTER, J. Craig et al.  
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
 WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 FILE REFERENCE: C1001307  
 CURRENT APPLICATION NUMBER: US/09/949,016  
 CURRENT FILING DATE: 2000-04-14  
 PRIOR APPLICATION NUMBER: 60/241,755  
 PRIOR FILING DATE: 2000-10-20  
 PRIOR APPLICATION NUMBER: 60/237,768  
 PRIOR FILING DATE: 2000-10-03  
 PRIOR APPLICATION NUMBER: 60/231,498  
 PRIOR FILING DATE: 2000-09-08  
 NUMBER OF SEQ ID NOS: 207012  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 8835  
 LENGTH: 506  
 TYPE: PRT

ORGANISM: Human  
 US-09-949-016-8835

Query Match 43.9%; Score 765; DB 2; Length 506;  
 Best Local Similarity 48.2%; Pred. No. 2.3e-72;  
 Matches 147; Conservative 59; Mismatches 89; Indels 10; Gaps 4;

QY 2 DRPLSVHLNGGKG--NRKTSCKPIKNOFGHFMKLDNSNYLLSKEYEELKQVGRNOS 58  
 DB 184 DYLLAFYINPWSKNGKLGKRLTNVQLDDPDAIYKDWAKSDYKFSLOFEBELKIGLDIP 243  
 QY 59 CDIALPENRGKRRYNNILPYDATRYKLSNVDDPCSDYINASYIPGNFRREYIYTOGP 118  
 DB 244 HPAADLPANCKRRYNNILPYDSFRVLYSNMBEGADYINANYIPGNSPOEYIATQGP 303  
 QY 119 LPTGKDDPMKRWMEQNVNINVTQCVEKRGYKCDHWYPADDSLYGDDLQWLSSEVYL 178  
 DB 304 LPTKNDPMKRWVWVLOKSOIIVMLQCNKRRYKCDHWYPTPEPIAYGDIIVEMISEEQ 363  
 QY 179 PEWTIREFKICEBOLDHRLIRHFTYTWPDHGV--ETTSLOIOPRTYRDYINRSPG 236  
 DB 364 DDMACRHFRI--NYADMQDVHFTYTPADHGVPTANAAESILQFVHWVROQATKS-- 418  
 QY 237 AGPTVHCSAGVGTGTFIALDRILQQLDSKDSVDIYGAVHDLRLHRYHNVOTECQYVL 296  
 DB 419 KGPMTIHCSAGVGTGTFIALDRILQHIRDHFVDILGLVSEMRSTRMSVOTEBQYIFI 478  
 QY 297 HOCVR 301  
 DB 479 HOCVQ 483

RESULT 13  
 US-09-949-016-8836  
 Sequence 8836, Application US/09949016  
 Patent No. 6812339  
 GENERAL INFORMATION:  
 APPLICANT: VENTER, J. Craig et al.  
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
 WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 FILE REFERENCE: C1001307  
 CURRENT APPLICATION NUMBER: US/09/949,016  
 CURRENT FILING DATE: 2000-04-14  
 PRIOR APPLICATION NUMBER: 60/241,755  
 PRIOR FILING DATE: 2000-10-20  
 PRIOR APPLICATION NUMBER: 60/237,768  
 PRIOR FILING DATE: 2000-10-03  
 PRIOR APPLICATION NUMBER: 60/231,498  
 PRIOR FILING DATE: 2000-09-08  
 NUMBER OF SEQ ID NOS: 207012  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 8836  
 LENGTH: 506  
 TYPE: PRT  
 ORGANISM: Human  
 US-09-949-016-8836

Query Match 43.9%; Score 765; DB 2; Length 506;  
 Best Local Similarity 48.2%; Pred. No. 2.3e-72;  
 Matches 147; Conservative 59; Mismatches 89; Indels 10; Gaps 4;

QY 2 DRPLSVHLNGGKG--NRKTSCKPIKNOFGHFMKLDNSNYLLSKEYEELKQVGRNOS 58  
 DB 184 DYLLAFYINPWSKNGKLGKRLTNVQLDDPDAIYKDWAKSDYKFSLOFEBELKIGLDIP 243  
 QY 59 CDIALPENRGKRRYNNILPYDATRYKLSNVDDPCSDYINASYIPGNFRREYIYTOGP 118  
 DB 244 HPAADLPANCKRRYNNILPYDSFRVLYSNMBEGADYINANYIPGNSPOEYIATQGP 303  
 QY 119 LPTGKDDPMKRWMEQNVNINVTQCVEKRGYKCDHWYPADDSLYGDDLQWLSSEVYL 178  
 DB 304 LPTKNDPMKRWVWVLOKSOIIVMLQCNKRRYKCDHWYPTPEPIAYGDIIVEMISEEQ 363

QY 179 PWTIRREKICGEQDARLIRHFTWPDHGV--ETTOSLQFRTVADYINRSPG 236  
 DB 364 DWACRHRRI---NYADEMODVMEHNTAMPDGVPTANNAESLQFVMTAQATKS-- 418  
 QY 237 AGPTVHCSAGVGRGTGFIALDRILQOLDSKDSVDIYGAVHDLRLHRYVMVOTECQVYL 296  
 DB 419 KGPMLIHCSAGVGRGTGFIALDRILQHIRDHEFVDILGLVSEKRSYRMSMVOTECQYIFI 478  
 QY 297 HOCVR 301  
 DB 479 HOCVQ 483

RESULT 14  
 US-09-949-016-8837

Sequence 8837, Application US/09949016  
 Patent No. 6812339  
 GENERAL INFORMATION:  
 APPLICANT: VENTER, J. Craig et al.  
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
 WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 FILE REFERENCE: C1001307  
 CURRENT APPLICATION NUMBER: US/09/949,016  
 PRIOR FILING DATE: 2000-04-14  
 PRIOR APPLICATION NUMBER: 60/241,755  
 PRIOR FILING DATE: 2000-10-20  
 PRIOR APPLICATION NUMBER: 60/237,768  
 PRIOR FILING DATE: 2000-10-03  
 PRIOR APPLICATION NUMBER: 60/231,498  
 PRIOR FILING DATE: 2000-09-08  
 NUMBER OF SEQ ID NOS: 207012  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 8837  
 LENGTH: 506  
 TYPE: PRT  
 ORGANISM: Human  
 US-09-949-016-8837

Query Match 43.9%; Score 765; DB 2; Length 506;  
 Best Local Similarity 48.2%; Pred. No. 2,3e-72;  
 Matches 147; Conservative 59; Mismatches 89; Indels 10; Gaps 4;

QY 2 DRPLSVHNLGQK---NKTSCPIKINOPEGHFMKLOADSNYLLSKEYEELKDVGRNQS 58  
 DB 184 DYLLAFYINPMSKXGKXKRLTNPVQLDDPDVAYIKDMAKSDYKFSLOPEELKJLGDIIP 243  
 QY 59 CDIALPEBKGRKRYNNILPYDATRYVLSVDDPCSDYINASYIPGNFRREYIVTQGP 118  
 DB 244 HPAADLPANRCKRNTNLPYDFSRVLYSMNEBEGADYINANYIGVNSPQEIYATQGP 303  
 QY 119 LFGTDQDFKRYMEQVAVNTVWVTCVEKRYKCHYVPADQDSLTYGDLILQMLSSVYL 178  
 DB 304 LPEIRNDPFWKMYLQOKSQIIVMLTQCNEKRYKCDHYMFTFEEPIAYGDIIVEMISEEQ 363  
 QY 179 PWTIRREKICGEQDARLIRHFTWPDHGV--ETTOSLQFRTVADYINRSPG 236  
 DB 364 DWACRHRRI---NYADEMODVMEHNTAMPDGVPTANNAESLQFVMTAQATKS-- 418  
 QY 237 AGPTVHCSAGVGRGTGFIALDRILQOLDSKDSVDIYGAVHDLRLHRYVMVOTECQVYL 296  
 DB 419 KGPMLIHCSAGVGRGTGFIALDRILQHIRDHEFVDILGLVSEKRSYRMSMVOTECQYIFI 478  
 QY 297 HOCVR 301  
 DB 479 HOCVQ 483

RESULT 15  
 US-09-949-016-8838  
 Sequence 8838, Application US/09949016  
 Patent No. 6812339  
 GENERAL INFORMATION:  
 APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
 WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 FILE REFERENCE: C1001307  
 CURRENT APPLICATION NUMBER: US/09/949,016  
 PRIOR FILING DATE: 2000-04-14  
 PRIOR APPLICATION NUMBER: 60/241,755  
 PRIOR FILING DATE: 2000-10-20  
 PRIOR APPLICATION NUMBER: 60/237,768  
 PRIOR FILING DATE: 2000-10-03  
 PRIOR APPLICATION NUMBER: 60/231,498  
 PRIOR FILING DATE: 2000-09-08  
 NUMBER OF SEQ ID NOS: 207012  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 8838  
 LENGTH: 506  
 TYPE: PRT  
 ORGANISM: Human  
 US-09-949-016-8838

Query Match 43.9%; Score 765; DB 2; Length 506;  
 Best Local Similarity 48.2%; Pred. No. 2,3e-72;  
 Matches 147; Conservative 59; Mismatches 89; Indels 10; Gaps 4;

QY 2 DRPLSVHNLGQK---NKTSCPIKINOPEGHFMKLOADSNYLLSKEYEELKDVGRNQS 58  
 DB 184 DYLLAFYINPMSKXGKXKRLTNPVQLDDPDVAYIKDMAKSDYKFSLOPEELKJLGDIIP 243  
 QY 59 CDIALPEBKGRKRYNNILPYDATRYVLSVDDPCSDYINASYIPGNFRREYIVTQGP 118  
 DB 244 HPAADLPANRCKRNTNLPYDFSRVLYSMNEBEGADYINANYIGVNSPQEIYATQGP 303  
 QY 119 LFGTDQDFKRYMEQVAVNTVWVTCVEKRYKCHYVPADQDSLTYGDLILQMLSSVYL 178  
 DB 304 LPEIRNDPFWKMYLQOKSQIIVMLTQCNEKRYKCDHYMFTFEEPIAYGDIIVEMISEEQ 363  
 QY 179 PWTIRREKICGEQDARLIRHFTWPDHGV--ETTOSLQFRTVADYINRSPG 236  
 DB 364 DWACRHRRI---NYADEMODVMEHNTAMPDGVPTANNAESLQFVMTAQATKS-- 418  
 QY 237 AGPTVHCSAGVGRGTGFIALDRILQOLDSKDSVDIYGAVHDLRLHRYVMVOTECQVYL 296  
 DB 419 KGPMLIHCSAGVGRGTGFIALDRILQHIRDHEFVDILGLVSEKRSYRMSMVOTECQYIFI 478  
 QY 297 HOCVR 301  
 DB 479 HOCVQ 483

Search completed: February 17, 2006, 01:26:31  
 Job time : 48 secs

ein search, using sw model

Run on: February 17, 2006, 01:36:29 ; Search time 165 Seconds  
(without alignments)

807.803 Million cell updates/sec

Title: US-10-634-027-7

Sequence: 1 GDRPLSVHLNLGQGNRKT...VRDVLRAKLRSEQHIIHHH 319

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Total number of hits satisfying chosen parameters: 1867565

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Minimum DB seq length: 0
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Post-processing:	Minimum Match 0%
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Listing first 45 summaries

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6/cgml_6/ptodataa/1/pubppaa/US11_PUBCOMB.pcp.*
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**pred.** No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1744	100.0	319	4	US-10-634-027-7	Sequence 7, Appl1
2	1691	97.0	336	4	US-10-634-027-4	Sequence 4, Appl1
3	1691	97.0	1997	3	US-09-909-567B-54	Sequence 54, Appl1
4	1691	97.0	1997	4	US-10-634-027-2	Sequence 2, Appl1
5	1691	97.0	1997	4	US-10-468-765A-2155	Sequence 215, Appl1
6	1691	97.0	1997	5	US-10-467-692-9	Sequence 4, Appl1
7	1691	97.0	1997	5	US-10-785-148-5168	Sequence 5168, Appl1
8	1690	96.9	312	4	US-10-634-027-6	Sequence 6, Appl1
9	1667	95.6	1450	5	US-10-467-692-14	Sequence 14, Appl1
10	1374	78.8	310	3	US-09-788-682-15	Sequence 15, Appl1
11	878.5	50.4	344	4	US-10-723-606-3	Sequence 3, Appl1
12	878.5	50.4	1337	4	US-10-350-501-2	Sequence 2, Appl1
13	878.5	50.4	1337	4	US-10-356-547-44	Sequence 42, Appl1
14	878.5	50.4	1337	4	US-10-356-547-42	Sequence 44, Appl1
15	878.5	50.4	1337	4	US-10-723-606-2	Sequence 2, Appl1
16	868.5	49.8	1238	4	US-10-366-547-49	Sequence 49, Appl1
17	868.5	49.8	1238	4	US-10-366-547-47	Sequence 47, Appl1
18	868.5	49.8	1647	6	US-11-037-140-2076	Sequence 2076, Appl1
19	829.5	47.6	1767	4	US-10-087-684-40	Sequence 40, Appl1
20	829.5	47.6	1767	4	US-10-218-779-48	Sequence 48, Appl1
21	829.5	47.6	1767	6	US-11-097-143-1970	Sequence 1470, Appl1
22	818.5	46.9	1767	4	US-10-087-684-41	Sequence 41, Appl1
23	818.5	46.9	1767	4	US-10-218-779-41	Sequence 41, Appl1
24	805.5	46.2	1447	5	US-10-467-692-13	Sequence 13, Appl1
25	768	44.7	405	5	US-10-029-345A-28	Sequence 28, Appl1
26	761.5	43.7	1188	4	US-10-331-496A-79	Sequence 79, Appl1
27	761.5	43.7	1188	4	US-10-789-241-34	Sequence 34, Appl1

## ALIGNMENTS

28	751.5	42.7	1188	5	US-10-029-1455-17	Sequence 27, Appl
29	744.5	42.7	1189	5	US-09-7828-626-26	Sequence 16, Appl
30	704.5	40.7	1093	4	US-10-245-539-4	Sequence 4, Appl
31	703.5	40.7	1118	4	US-10-245-539-2	Sequence 2, Appl
32	703.5	40.7	1118	4	US-10-245-539-8	Sequence 8, Appl
33	701	40.2	1367	4	US-10-369-693-5508	Sequence 508, Appl
34	701	40.2	1367	4	US-10-369-693-5509	Sequence 509, Appl
35	697.5	40.7	1711	5	US-09-822-4454-38	Sequence 38, Appl
36	675	38.7	2301	5	US-09-822-871-1	Sequence 4, Appl
37	675	38.7	2301	4	US-10-673-685-4	Sequence 4, Appl
38	675	38.7	2302	4	US-10-087-684-37	Sequence 37, Appl
39	675	38.7	2302	4	US-10-218-779-37	Sequence 37, Appl
40	673.5	38.6	1705	4	US-10-029-5454-37	Sequence 37, Appl
41	673	38.6	401	4	US-10-314-332-15	Sequence 15, Appl
42	673	38.6	898	4	US-10-314-332-22	Sequence 22, Appl
43	673	38.6	2299	4	US-10-466-159-2	Sequence 2, Appl
44	673	38.6	2300	4	US-10-087-684-10	Sequence 10, Appl
45	673	38.6	2300	4	US-10-218-779-10	Sequence 10, Appl

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1  RESULT 1
2  US-10-634-027-7
3  / Sequence 7, Application US/10634027
4  / Publication No. US20040077065A1
5  /
6  / GENERAL INFORMATION:
7  /
8  / APPLICANT: Picoter & Gamble Company
9  /
10 / APPLICANT: ENKOLNOV, Artem A
11 / APPLICANT: ENKOLNOV, Mattheo E
12 /
13 / FILING REFERENCE: 9045548
14 /
15 / CURRENT APPLICATION NUMBER: US/10/634, 027
16 /
17 / CURRENT FILING DATE: 2003-08-04
18 /
19 / PRIOR APPLICATION NUMBER: US 60/413,547
20 /
21 / PRIOR FILING DATE: 2002-09-25
22 /
23 / NUMBER OF SEQ ID NOS: 15
24 /
25 / SOFTWARE: Patentin version 3.2
26 /
27 / SEQ ID NO 7
28 /
29 / LENGTH: 319
30 /
31 / TYPE: PRT
32 /
33 / ORGANISM: Homo sapiens
34 /
35 / US-10-634-027-7

```

Query Match	Score	DB 4	Length
100.0%	1744		319
Best Local Similarity	Pred. No. 2,3e-158		

Matches 319; Conservative 0; Indels 0; Gaps 0

1 GNRPLSVHNLGQKGNKTSICPIKINQFGHFMKLQADSNYLLSKEYEELDVGRNQCD 60

Db - 1 GDRPLSVHLNGQGNRKTCPIKINQFEGRFMKLDADSNYLLSKEYEELKDVGRRQSCD 60

61 IALLPENCKRRYNNILPYDATRVKLSNVDDPCSDYINASYTPGNFRREYIVTQBLP 120

Db 61 IALLPENGKRNINILPYDATRVKLSNVDDPCSDYINASYIPGNRRREYIVTQPLP 120

121 GTKDDFWKRWMEONTNINIWMITQCEVEKGRYKCDHYWPAQDSLYYGDLILOMLSESVLPE 180

Db 121 GTKDDFWKMMWEQNVHNI VAWTQCVEKGRVCDHYWPADQDSL YGDIILQMLSESVLPE 180

181 WTIREFKIGEEQLDAHRLRHFHVTWMDHGVPETTSLLIQVRTVRDYINRSPGAGPT 240

Db 181 WTIEFKICGEEQDAHRLRHFFHYTWPDHGVPETQSLIQFVRYRDYINRSPGAGPT 240

241 VVHCSAGVGTGTFIALDRILQQLDSKDSVDIYGAVHDLRLHVMVQTEQYVYLHOCV 300

Db 241 VTHSAGVGRTGTFIALDRILQQLDSKSDYDIYGAVHDLRLRVNHVQTECQYYLHQCV 300

301 RDVLRAKLRSEQHIIHHH 319

Db 301 RDVLPARKLRSEOHNNHHH 319



```

RESULT 2
US-10-634-027-4
; Sequence 4, Application US/10634027
; Publication No. US20040077065A1
GENERAL INFORMATION:
APPLICANT: Procter & Gamble Company
APPLICANT: Evdokimov, Artem G
APPLICANT: Pokrowsky, Matthew E
TITLE OF INVENTION: Three Dimensional Coordinates of HPTbeta
FILE REFERENCE: 904SM2
CURRENT APPLICATION NUMBER: US/10/634,027
CURRENT FILING DATE: 2003-08-04
PRIOR APPLICATION NUMBER: US 60/413,547
PRIOR FILING DATE: 2002-09-25
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.2
SEQ ID NO: 4
LENGTH: 336
TYPE: PRT
ORGANISM: Homo sapiens
US-10-634-027-4

Query Match          97.0%; Score 1691; DB 4; Length 336;
Best Local Similarity 99.4%; Pred. No. 2,9e+153;
Matches 312; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 DRPSVHNLGGCKNGRTRSPKIKINQFGCHMKLOADSNVYLSTKEVEELKDVGNGSCDI 61
        |||
DB       1 DRPSVHNLGGCKNGRTRSPKIKINQFGCHMKLOADSNVYLSTKEVEELKDVGNGSCDI 60

QY      62 ALLENRGKNRYNNILPYDTRYKLSTNDDPCSDYTINASTIPENNFRRETYVTQGPLG 121
        |||
DB       61 ALLENRGKNRYNNILPYDTRYKLSTNDDPCSDYTINASTIPENNFRRETYVTQGPLG 120

QY      122 TKQDFPMWMEQNEVNIWMTQTCVEKGKVKCDHYMPADDSLYYGDLLIOMLSSVLPEM 181
        |||
DB       121 TKQDFPMWMEQNEVNIWMTQTCVEKGKVKCDHYMPADDSLYYGDLLIOMLSSVLPEM 180

QY      182 TIRPFKICEEQLDAHLIRHFHYTVMPDHGVPETQSIIQFATVDYDYNKSGAGPTV 241
        |||
DB       181 TIRPFKICEEQLDAHLIRHFHYTVMPDHGVPETQSIIQFATVDYDYNKSGAGPTV 240

QY      242 VHSAGVGTGFALRLRIQQGLSKDSVDIDYGAVHDLELRHVMMQTFCQYVLIHQCYR 301
        |||
DB       241 VHSAGVGTGFALRLRIQQGLSKDSVDIDYGAVHDLELRHVMMQTFCQYVLIHQCYR 300

QY      302 DYLAARKLSROHH 315
        |||
DB       301 DYLAARKLSROEH 314

RESULT 3
US-09-909-567B-54
Sequence 54, Application US/09909567B
Publication No. US20030022257A1
GENERAL INFORMATION:
APPLICANT: Macina, Roberto A.
APPLICANT: Nair, Manoj
APPLICANT: Chen, Selva
TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes
FILE REFERENCE: DEX-0214
CURRENT APPLICATION NUMBER: US/09/909,567B
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: 60/219,834
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 54
LENGTH: 1997
TYPE: PRT
ORGANISM: Homo sapien
US-09-909-567B-54
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Query	Macc	Similarity	97.0%	Score	1691	DB 3	Length	1997
Best Local	Similarity	97.4%	Pred. No.	3.3e-152				
Matches	312	Conservative	1	Mismatches	1	Indels	0	Gaps
Qy	2	DBPLSVHNLGQKNGKRTSCPIKINQEGHPFKLQADSNVLSKYEELKDVGKNGSCDI	61					
Db	1662	DBPLSVHNLGQKNGKRTSCPIKINQEGHPFKLQADSNVLSKYEELKDVGKNGSCDI	1722					
Qy	62	ALPBNNGKRRNNILPYATRYVLSNVDDPCSDYINASYIPGNFRREYIVTQGPLG	121					
Db	1722	ALPBNNGKRRNNILPYATRYVLSNVDDPCSDYINASYIPGNFRREYIVTQGPLG	1781					
Qy	122	TQDFPMQWQBEQNVHNIWVWTCVEKGRKCDHWPADODSLYGDILLQMLSESULPEM	181					
Db	1782	TQDFPMQWQBEQNVHNIWVWTCVEKGRKCDHWPADODSLYGDILLQMLSESULPEM	1841					
Qy	182	TTRFKICGEBOLDARHLIRHRYVTWPDHGVPEITQSLIQFRTVADYINSPGAPGV	241					
Db	1842	TTRFKICGEBOLDARHLIRHRYVTWPDHGVPEITQSLIQFRTVADYINSPGAPGV	1901					
Qy	242	VHCSAGVGRGTFIALDRILQODSKDSVDYIGAVHDLRHHVHWQTECOYVLIHOCVR	301					
Db	1902	VHCSAGVGRGTFIALDRILQODSKDSVDYIGAVHDLRHHVHWQTECOYVLIHOCVR	1961					
Qy	302	DYLSARKLSRQOH	315					
Db	1962	DYLSARKLSRQOH	1975					
RESULT 4								
US-10-634-027-2								
Sequence 2, Application US/10634027								
Publication No. US20040077065A1								
GENERAL INFORMATION:								
APPLICANT: Procter & Gamble Company								
APPLICANT: Evdokimov, Mattheu E								
APPLICANT: Pokrosz, Mattheu E								
TITLE OF INVENTION: Three Dimensional Coordinates of Hprtbeta								
FILE REFERENCE: 9045M2								
CURRENT APPLICATION NUMBER: US/10/634, 027								
CURRENT FILING DATE: 2003-08-04								
PRIOR APPLICATION NUMBER: US 60/413,547								
PRIOR FILING DATE: 2002-09-25								
NUMBER OF SEQ ID NOS: 15								
SOFTWARE: PatentIn version 3.2								
SEQ ID NO 2								
LENGTH: 1997								
TYPE: PRT								
ORGANISM: Homo sapiens								
US-10-634-027-2								
Query Match	97.0%	Score 1691	DB 4	Length 1997				
Best Local Similarity	99.4%	Pred. No. 3.3e-152						
Matches 312	Conservative	1	Mismatches	1	Indels	0	Gaps	0
Qy	2	DBPLSVHNLGQKNGKRTSCPIKINQEGHPFKLQADSNVLSKYEELKDVGKNGSCDI	61					
Db	1662	DBPLSVHNLGQKNGKRTSCPIKINQEGHPFKLQADSNVLSKYEELKDVGKNGSCDI	1721					
Qy	62	ALPBNNGKRRNNILPYATRYVLSNVDDPCSDYINASYIPGNFRREYIVTQGPLG	121					
Db	1722	ALPBNNGKRRNNILPYATRYVLSNVDDPCSDYINASYIPGNFRREYIVTQGPLG	1781					
Qy	122	TQDFPMQWQBEQNVHNIWVWTCVEKGRKCDHWPADODSLYGDILLQMLSESULPEM	181					
Db	1782	TQDFPMQWQBEQNVHNIWVWTCVEKGRKCDHWPADODSLYGDILLQMLSESULPEM	1841					
Qy	182	TTRFKICGEBOLDARHLIRHRYVTWPDHGVPEITQSLIQFRTVADYINSPGAPGV	241					
Db	1842	TTRFKICGEBOLDARHLIRHRYVTWPDHGVPEITQSLIQFRTVADYINSPGAPGV	1901					
Qy	242	VHCSAGVGRGTFIALDRILQODSKDSVDYIGAVHDLRHHVHWQTECOYVLIHOCVR	301					
Db	1902	VHCSAGVGRGTFIALDRILQODSKDSVDYIGAVHDLRHHVHWQTECOYVLIHOCVR	1961					
Qy	302	DYLSARKLSRQOH	315					
Db	1962	DYLSARKLSRQOH	1975					

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Db      1902 VHSASVGRGTGFIALDRILLOQDSKSDVDIYGAVHDLRLHRVAVQTECOYVYLHQCVR 1961
Qy      302 DVLRARKLRSEOH 315
Db      1962 DVLRARKLRSEOH 1975

RESULT 5
US-10-408-765A-2135
; Sequence 2135, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Boin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Marnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 650088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: Pat-Seq for Windows Version 4.0
; SEQ ID NO 2135
; LENGTH: 1997
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-2135

Query Match      97.0%; Score 1691; DB 4; Length 1997;
Best Local Similarity 99.4%; Pred. No. 3.3e-152;
Matches 312; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      2 DRPLSVHNLGQKGNKRTSCPIKINQFEGHFMKLQADSNYLLSKYEYELKDVGRNOSCDI 61
Db      1662 DRPLSVHNLGQKGNKRTSCPIKINQFEGHFMKLQADSNYLLSKYEYELKDVGRNOSCDI 1721
Qy      62 ALPENRGKRNYYNLLPYDATRVKLSNVDDPCSDYINASYIPGNFRREYIVTGGPLPG 121
Db      1722 ALPENRGKRNYYNLLPYDATRVKLSNVDDPCSDYINASYIPGNFRREYIVTGGPLPG 1781
Qy      122 TKDDFKMVMWQWVNHNIWVWTCVKGKRVKCDHYMPADODSLYYGDLILQMSSEVLPFW 181
Db      1782 TKDDFKMVMWQWVNHNIWVWTCVKGKRVKCDHYMPADODSLYYGDLILQMSSEVLPFW 1841
Qy      182 TTRFKICGEQDLARLIRHRYTWPDHGVEPTTOSLIQFVATRVYDINNSPGAGPTV 241
Db      1842 TTRFKICGEQDLARLIRHRYTWPDHGVEPTTOSLIQFVATRVYDINNSPGAGPTV 1901
Qy      242 VHSASVGRGTGFIALDRILLOQDSKSDVDIYGAVHDLRLHRVAVQTECOYVYLHQCVR 301
Db      1902 VHSASVGRGTGFIALDRILLOQDSKSDVDIYGAVHDLRLHRVAVQTECOYVYLHQCVR 1961
Qy      302 DVLRARKLRSEOH 315
Db      1962 DVLRARKLRSEOH 1975

RESULT 6
US-10-497-692-4
; Sequence 4, Application US/10497692
; Publication No. US2005004056A1
; GENERAL INFORMATION:
; APPLICANT: Meise, Martin
; APPLICANT: Eulenberg, Karsten
; APPLICANT: Fritsch, Rudiger
; APPLICANT: Hader, Thomas
; APPLICANT: Bromer, Gunter
; APPLICANT: Steuernagel, Arnd

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; TITLE OF INVENTION: Prp10d, Tec protein tyrosine kinase and EDRP homologous protei
; TITLE OF INVENTION: Involved in the regulation of energy homeostasis
; FILE REFERENCE: 2923-632
; CURRENT APPLICATION NUMBER: US/10/497,692
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: PCT/EP02/13744
; PRIOR FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: EP 01 000 010.5
; PRIOR FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: EP 01 129 138.2
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: EP 01 128 844.6
; PRIOR FILING DATE: 2001-12-04
; SOFTWARE: Patent version 3.2
; NUMBER OF SEQ ID NOS: 20
; SEQ ID NO 4
; LENGTH: 1997
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-497-692-4

Query Match      97.0%; Score 1691; DB 5; Length 1997;
Best Local Similarity 99.4%; Pred. No. 3.3e-152;
Matches 312; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      2 DRPLSVHNLGQKGNKRTSCPIKINQFEGHFMKLQADSNYLLSKYEYELKDVGRNOSCDI 61
Db      1662 DRPLSVHNLGQKGNKRTSCPIKINQFEGHFMKLQADSNYLLSKYEYELKDVGRNOSCDI 1721
Qy      62 ALPENRGKRNYYNLLPYDATRVKLSNVDDPCSDYINASYIPGNFRREYIVTGGPLPG 121
Db      1722 ALPENRGKRNYYNLLPYDATRVKLSNVDDPCSDYINASYIPGNFRREYIVTGGPLPG 1781
Qy      122 TKDDFKMVMWQWVNHNIWVWTCVKGKRVKCDHYMPADODSLYYGDLILQMSSEVLPFW 181
Db      1782 TKDDFKMVMWQWVNHNIWVWTCVKGKRVKCDHYMPADODSLYYGDLILQMSSEVLPFW 1841
Qy      182 TTRFKICGEQDLARLIRHRYTWPDHGVEPTTOSLIQFVATRVYDINNSPGAGPTV 241
Db      1842 TTRFKICGEQDLARLIRHRYTWPDHGVEPTTOSLIQFVATRVYDINNSPGAGPTV 1901
Qy      242 VHSASVGRGTGFIALDRILLOQDSKSDVDIYGAVHDLRLHRVAVQTECOYVYLHQCVR 301
Db      1902 VHSASVGRGTGFIALDRILLOQDSKSDVDIYGAVHDLRLHRVAVQTECOYVYLHQCVR 1961
Qy      302 DVLRARKLRSEOH 315
Db      1962 DVLRARKLRSEOH 1975

RESULT 7
US-10-756-149-5168
; Sequence 5168, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Zlotnik, Albert
; APPLICANT: Aiziz, Nabasha
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER. COMPOSITIONS
; TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/756,149
; CURRENT FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: Patent version 3.2
; SEQ ID NO 5168
; LENGTH: 1997
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-756-149-5168

Query Match      97.0%; Score 1691; DB 5; Length 1997;
Best Local Similarity 99.4%; Pred. No. 3.3e-152;
Matches 312; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy 2 DRPLSVHLNIGQKGRKTSCTPKINOFEGHFMKLOADSNVLSKEYEELKDVGKNSCDI 61
Db 1662 DRPLSVHLNIGQKGRKTSCTPKINOFEGHFMKLOADSNVLSKEYEELKDVGKNSCDI 1721
Qy 62 ALLEPENGKRRNNILPYDATRVKLSNVDDPCSDYINNSYIPGNPFREYITVTOGPIRG 121
Db 1722 ALLEPENGKRRNNILPYDATRVKLSNVDDPCSDYINNSYIPGNPFREYITVTOGPIRG 1781
Qy 122 TKDDPFWMEQWQVNIWMTQCEKGRKCDHYWPAADDSLYGDLILQMLSESVLPFW 181
Db 1782 TKDDPFWMEQWQVNIWMTQCEKGRKCDHYWPAADDSLYGDLILQMLSESVLPFW 1841
Qy 182 TIRFEFKICGEBOLDARLIRHFHYTWPDHGVPTTOSLIQFVRTVRDYINRSPGAGPTV 241
Db 1842 TIRFEFKICGEBOLDARLIRHFHYTWPDHGVPTTOSLIQFVRTVRDYINRSPGAGPTV 1901
Qy 242 VHCASAGVGRGTFIALDRILQOQDSKDSVDIYGAVHDLRLHVRVWQTECOVYVYLHQCVR 301
Db 1902 VHCASAGVGRGTFIALDRILQOQDSKDSVDIYGAVHDLRLHVRVWQTECOVYVYLHQCVR 1961
Qy 302 DVLRARKLRSEQH 315
Db 1962 DVLRARKLRSEQH 1975

RESULT 8
US-10-634-027-6
; Sequence 6, Application US/10634027
; Publication No. US20040077065M1
; GENERAL INFORMATION:
; APPLICANT: Procter & Gamble Company
; APPLICANT: Evdokimov, Artem G
; APPLICANT: Pokros, Matthew B
; TITLE OF INVENTION: Three Dimensional Coordinates of HPTpbeta
; FILE REFERENCE: 9045M2
; CURRENT APPLICATION NUMBER: US/10/634,027
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 60/413,547
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-634-027-6

Query Match 96.9%; Score 1690; DB 4; Length 312;
Best Local Similarity 100.0%; Pred. No. 3.3e-153;
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DRPLSVHLNIGQKGRKTSCTPKINOFEGHFMKLOADSNVLSKEYEELKDVGKNSCDI 61
Db 1 DRPLSVHLNIGQKGRKTSCTPKINOFEGHFMKLOADSNVLSKEYEELKDVGKNSCDI 60
Qy 62 ALLEPENGKRRNNILPYDATRVKLSNVDDPCSDYINNSYIPGNPFREYITVTOGPIRG 121
Db 61 ALLEPENGKRRNNILPYDATRVKLSNVDDPCSDYINNSYIPGNPFREYITVTOGPIRG 120
Qy 122 TKDDPFWMEQWQVNIWMTQCEKGRKCDHYWPAADDSLYGDLILQMLSESVLPFW 181
Db 121 TKDDPFWMEQWQVNIWMTQCEKGRKCDHYWPAADDSLYGDLILQMLSESVLPFW 180
Qy 182 TIRFEFKICGEBOLDARLIRHFHYTWPDHGVPTTOSLIQFVRTVRDYINRSPGAGPTV 241
Db 181 TIRFEFKICGEBOLDARLIRHFHYTWPDHGVPTTOSLIQFVRTVRDYINRSPGAGPTV 240
Qy 242 VHCASAGVGRGTFIALDRILQOQDSKDSVDIYGAVHDLRLHVRVWQTECOVYVYLHQCVR 301
Db 241 VHCASAGVGRGTFIALDRILQOQDSKDSVDIYGAVHDLRLHVRVWQTECOVYVYLHQCVR 300
Qy 302 DVLRARKLRSEQ 313

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Db 301 DVLRARKLRSEQ 312

RESULT 9
US-10-497-692-14
; Sequence 14, Application US/10497692
; Publication No. US20050004056M1
; GENERAL INFORMATION:
; APPLICANT: Meise, Martin
; APPLICANT: Eulenberg, Karsten
; APPLICANT: Fritsch, Rudiger
; APPLICANT: Hader, Thomas
; APPLICANT: Bromner, Gunter
; APPLICANT: Steierhagel, Arnd
; TITLE OF INVENTION: Ept10D, Tec protein tyrosine kinase and EPT1 homologous protein
; FILE REFERENCE: 2923-632
; CURRENT APPLICATION NUMBER: US/10/497,692
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: PCT/EP02/13744
; PRIOR FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: EP 01 000 010.5
; PRIOR FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: EP 01 129 138.2
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: EP 01 128 844.6
; PRIOR FILING DATE: 2001-12-04
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 1450
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-497-692-14

Query Match 95.6%; Score 1667; DB 5; Length 1450;
Best Local Similarity 100.0%; Pred. No. 4.2e-150;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DRPLSVHLNIGQKGRKTSCTPKINOFEGHFMKLOADSNVLSKEYEELKDVGKNSCDI 61
Db 1144 DRPLSVHLNIGQKGRKTSCTPKINOFEGHFMKLOADSNVLSKEYEELKDVGKNSCDI 1203
Qy 62 ALLEPENGKRRNNILPYDATRVKLSNVDDPCSDYINNSYIPGNPFREYITVTOGPIRG 121
Db 1204 ALLEPENGKRRNNILPYDATRVKLSNVDDPCSDYINNSYIPGNPFREYITVTOGPIRG 1263
Qy 122 TKDDPFWMEQWQVNIWMTQCEKGRKCDHYWPAADDSLYGDLILQMLSESVLPFW 181
Db 1264 TKDDPFWMEQWQVNIWMTQCEKGRKCDHYWPAADDSLYGDLILQMLSESVLPFW 1323
Qy 182 TIRFEFKICGEBOLDARLIRHFHYTWPDHGVPTTOSLIQFVRTVRDYINRSPGAGPTV 241
Db 1324 TIRFEFKICGEBOLDARLIRHFHYTWPDHGVPTTOSLIQFVRTVRDYINRSPGAGPTV 1383
Qy 242 VHCASAGVGRGTFIALDRILQOQDSKDSVDIYGAVHDLRLHVRVWQTECOVYVYLHQCVR 301
Db 1384 VHCASAGVGRGTFIALDRILQOQDSKDSVDIYGAVHDLRLHVRVWQTECOVYVYLHQCVR 1443
Qy 302 DVLRARK 308
Db 1444 DVLRARK 1450

RESULT 10
US-09-788-626-15
; Sequence 15, Application US/09788626
; Patent No. US20020009762M1
; GENERAL INFORMATION:
; APPLICANT: Piant, Andrew J.
; APPLICANT: Cool, Deborah E.
; TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE

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TITLE OF INVENTION: PHOSPHATASES  
 FILE REFERENCE: 200125.401  
 CURRENT APPLICATION NUMBER: US/09/786,626  
 CURRENT FILING DATE: 2001-02-13  
 NUMBER OF SEQ ID NOS: 40  
 SOFTWARE: FASTSEQ for Windows Version 4.0  
 SEQ ID NO 15  
 LENGTH: 310  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-786-626-15

Query Match 78.8%; Score 1374; DB 3; Length 310;  
 Best Local Similarity 99.2%; Pred. No. 6,4e-123;  
 Matches 254; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 56 NOSCIALLPENRGRKRNINILPYDATTRVLSVDDDCSDYINASYIPGNFRREYIVT 115  
 DB 1 NOSCIALLPENRGRKRNINILPYDATTRVLSVDDDCSDYINASYIPGNFRREYIVT 60  
 QY 116 OGPFGCTDDPMKMWKQWQVNHVWVQCVKGRYKCDHWPADQSLYYGDLILQMLSE 175  
 DB 61 OGPFGCTDDPMKMWKQWQVNHVWVQCVKGRYKCDHWPADQSLYYGDLILQMLSE 120  
 QY 176 SVLPETITREKTCGSEQLDARLIRHPTTWPBGHVPETTSLOFVTRVRYINRSP 235  
 DB 121 SVLPETIT--FKLCGSEQLDARLIRHPTTWPBGHVPETTSLOFVTRVRYINRSP 178  
 QY 236 GAGPTVWCHSAGVGRGTFTIALDRILQDLSDKSDYDIGAVHDLRLHRYHWQTECYIVT 295  
 DB 179 GAGPTVWCHSAGVGRGTFTIALDRILQDLSDKSDYDIGAVHDLRLHRYHWQTECYIVT 238  
 QY 296 LHCQVRDYLARKLRS 311  
 DB 239 LHCQVRDYLARKLRS 254

RESULT 11  
 US-10-723-606-3  
 Sequence 3, Application US/10723606  
 Publication No. US20040161821A1  
 GENERAL INFORMATION:  
 APPLICANT: Tonks, Nicholas K.  
 TITLE OF INVENTION: DEP-1 RECEPTOR PROTEIN TYROSINE  
 TITLE OF INVENTION: PHOSPHATASE INTERACTING PROTEINS  
 TITLE OF INVENTION: AND RELATED METHODS  
 FILE REFERENCE: 200125.447  
 CURRENT APPLICATION NUMBER: US/10/723,606  
 CURRENT FILING DATE: 2003-11-26  
 NUMBER OF SEQ ID NOS: 22  
 SOFTWARE: FASTSEQ for Windows Version 4.0  
 SEQ ID NO 3  
 LENGTH: 341  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-723-606-3

Query Match 50.4%; Score 878.5; DB 4; Length 341;  
 Best Local Similarity 56.4%; Pred. No. 2.3e-75;  
 Matches 164; Conservative 56; Mismatches 68; Indels 3; Gaps 3;

QY 18 KTSCKIKNOFEGHFKLQADSNYLSKEYEELKDVGNOSCIALLPENRGRKRNINIL 77  
 DB 20 KTSCKIKNEFEAYFKKQOQDSNGCFABEYEDKLVGISQPKYAALANRGRKRNINIL 79  
 QY 78 PYDATRVKLSNVDDPCSDYINASYIPGNFRREYIVTQGLPGTDDPMKMWKQWQVNH 137  
 DB 80 PYDISRVKLS-VQTHSTDDYINAVYMGYSKDDFIATQGLPNTLKDFWMEKKNVYA 138  
 QY 138 IYMTQCVKGRYKCDHWPADQSLYYGDLILQMLSESVLPETITREKTCGSEQLDAH 197  
 DB 139 IYMTKCVKGRYKCDHWPADQSLYYGDLILQMLSESVLPETITREKTCGSEQLDAH 197

QY 198 RLIRHPTTWPBGHVPETTSLOFVTRVRYINRSPGAGPTVWCHSAGVGRGTFTIAL 257  
 DB 198 PL-RQHFTSWPDHGVDDTDLINFRYLVRDYMKSPPESPLVHCSAGVGRGTFTIAL 256  
 QY 258 DRILQDLSDKSDYDIGAVHDLRLHRYHWQTECYIVTLCQVRDYLARK 308  
 DB 257 DRILQDLSDKSDYDIGAVHDLRLHRYHWQTECYIVTLCQVRDYLARK 307

RESULT 12  
 US-10-390-501-2  
 Sequence 2, Application US/10390501  
 Publication No. US20030148491A1  
 GENERAL INFORMATION:  
 APPLICANT: Tonks, Nicholas K.  
 TITLE OF INVENTION: DENSITY ENHANCED PROTEIN TYROSINE  
 PHOSPHATASES  
 NUMBER OF SEQUENCES: 6  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Seed IP Law Group PLLC  
 STREET: Suite 6300, 701 Fifth Avenue  
 CITY: Seattle  
 STATE: Washington  
 COUNTRY: USA  
 ZIP: 98104  
 COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA: US/10/390,501  
 APPLICATION NUMBER: US/10/390,501  
 FILING DATE: 13-Mar-2003  
 CLASSIFICATION: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Roseman Ph.D., Stephen J.  
 REGISTRATION NUMBER: 43,058  
 REFERENCE/DOCKET NUMBER: 200125.402C2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (206) 682-4900  
 TELEFAX: (206) 682-6031  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1337 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 US-10-390-501-2

Query Match 50.4%; Score 878.5; DB 4; Length 1337;  
 Best Local Similarity 56.4%; Pred. No. 1.4e-74;  
 Matches 164; Conservative 56; Mismatches 68; Indels 3; Gaps 3;

QY 18 KTSCKIKNOFEGHFKLQADSNYLSKEYEELKDVGNOSCIALLPENRGRKRNINIL 77  
 DB 1016 KTSCKIKRYNEAEAFKKQOQDSNGCFABEYEDKLVGISQPKYAALANRGRKRNINIL 1075  
 QY 78 PYDATRVKLSNVDDPCSDYINASYIPGNFRREYIVTQGLPGTDDPMKMWKQWQVNH 137  
 DB 1076 PYDISRVKLS-VQTHSTDDYINAVYMGYSKDDFIATQGLPNTLKDFWMEKKNVYA 1134  
 QY 138 IYMTQCVKGRYKCDHWPADQSLYYGDLILQMLSESVLPETITREKTCGSEQLDAH 197  
 DB 1135 IYMTKCVKGRYKCDHWPADQSLYYGDLILQMLSESVLPETITREKTCGSEQLDAH 193  
 QY 198 RLIRHPTTWPBGHVPETTSLOFVTRVRYINRSPGAGPTVWCHSAGVGRGTFTIAL 257  
 DB 1194 PL-RQHFTSWPDHGVDDTDLINFRYLVRDYMKSPPESPLVHCSAGVGRGTFTIAL 1252  
 QY 258 DRILQDLSDKSDYDIGAVHDLRLHRYHWQTECYIVTLCQVRDYLARK 308

DB 1253 DRLIYQIENNTVDYGIYDLRMHRPLMWQTEDOYVFLNQCVDIVASOK 1303

## RESULT 13

US-10-366-547-42  
 ; Sequence 42, Application US/10366547  
 ; Publication No. US20030215899A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Meng, Tzu-Ching  
 ; APPLICANT: Tonks, Nicholas K.  
 ; APPLICANT: Cool, Deborah B.  
 ; TITLE OF INVENTION: REVERSIBLE OXIDATION OF PROTEIN TYROSINE  
 ; FILE REFERENCE: 200125, 439  
 ; CURRENT APPLICATION NUMBER: US/10/366,547  
 ; CURRENT FILING DATE: 2003-02-12  
 ; NUMBER OF SEQ ID NOS: 98  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 42  
 ; LENGTH: 1337  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-366-547-42

Query Match 50.4%; Score 878.5; DB 4; Length 1337;  
 Best Local Similarity 56.4%; Pred. No. 1.4e-74;  
 Matches 164; Conservative 56; Mismatches 68; Indels 3; Gaps 3;

QY 18 KTSCPIKINQFESHPKLOADSNLYLSKEYEELKDVGRNOSCDIALLENNNGKRRYNNIL 77  
 DB 1016 KSKSLIRVENFEAYFFKQOADSNGRAEYEDLKVGISQPKYALLENKGRNRNNVL 1075  
 QY 78 PYDATRYVLSNVDDPCSDYINASYIPGNFRREYIVTQGLPGLTKDPFWKRWMEONVAN 137  
 DB 1076 PYDISRVKLS-VQTHSTDDYINANVMPGYHSKQFIATQGLPLENTLKDFMWRWENKRVYA 1134  
 QY 138 IVMVTCQVEKGRKCDHYMPADQPSLYGDLILQMLSESYLPEWTIRREFKICGEQOLDAN 197  
 DB 1133 IIMTKCEVGRKCEYWPSPKQ-AQDYGDIVAMTSEIVLPEWTIRDFYKNIQTSSEH 1193  
 QY 198 RLIRHFHYTWPDHGPVETTSQSLIOFRTVRDYINRSPGAPTVVHCAGVGRGTGFIAL 257  
 DB 1194 PL-RQFHTSMRPHGVPDTDLINFRYLVRDYWKQSPSPSFLVHCAGVGRGTGFIAL 1252  
 QY 258 DRLIQQDSDSDYDIYGAVHDLRLHRVHWVQTECOYVYLHQCVRDVLARK 308  
 DB 1253 DRLIYQIENNTVDYGIYDLRMHRPLMWQTEDOYVFLNQCVDIVASOK 1303

## RESULT 14

US-10-366-547-44  
 ; Sequence 44, Application US/10366547  
 ; Publication No. US20030215899A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Meng, Tzu-Ching  
 ; APPLICANT: Tonks, Nicholas K.  
 ; APPLICANT: Cool, Deborah B.  
 ; TITLE OF INVENTION: REVERSIBLE OXIDATION OF PROTEIN TYROSINE  
 ; FILE REFERENCE: 200125, 439  
 ; CURRENT APPLICATION NUMBER: US/10/366,547  
 ; CURRENT FILING DATE: 2003-02-12  
 ; NUMBER OF SEQ ID NOS: 98  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 44  
 ; LENGTH: 1337  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-366-547-44

Query Match 50.4%; Score 878.5; DB 4; Length 1337;  
 Best Local Similarity 56.4%; Pred. No. 1.4e-74;

Matches 164; Conservative 56; Mismatches 68; Indels 3; Gaps 3;  
 QY 18 KTSCPIKINQFESHPKLOADSNLYLSKEYEELKDVGRNOSCDIALLENNNGKRRYNNIL 77  
 DB 1016 KSKSLIRVENFEAYFFKQOADSNGRAEYEDLKVGISQPKYALLENKGRNRNNVL 1075  
 QY 78 PYDATRYVLSNVDDPCSDYINASYIPGNFRREYIVTQGLPGLTKDPFWKRWMEONVAN 137  
 DB 1076 PYDISRVKLS-VQTHSTDDYINANVMPGYHSKQFIATQGLPLENTLKDFMWRWENKRVYA 1134  
 QY 138 IVMVTCQVEKGRKCDHYMPADQPSLYGDLILQMLSESYLPEWTIRREFKICGEQOLDAN 197  
 DB 1133 IIMTKCEVGRKCEYWPSPKQ-AQDYGDIVAMTSEIVLPEWTIRDFYKNIQTSSEH 1193  
 QY 198 RLIRHFHYTWPDHGPVETTSQSLIOFRTVRDYINRSPGAPTVVHCAGVGRGTGFIAL 257  
 DB 1194 PL-RQFHTSMRPHGVPDTDLINFRYLVRDYWKQSPSPSFLVHCAGVGRGTGFIAL 1252  
 QY 258 DRLIQQDSDSDYDIYGAVHDLRLHRVHWVQTECOYVYLHQCVRDVLARK 308  
 DB 1253 DRLIYQIENNTVDYGIYDLRMHRPLMWQTEDOYVFLNQCVDIVASOK 1303

## RESULT 15

US-10-723-606-2  
 ; Sequence 2, Application US/10723606  
 ; Publication No. US20040161821A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Palka-Hamblin, Helena L.  
 ; APPLICANT: Tonks, Nicholas K.  
 ; TITLE OF INVENTION: DEP-1 RECEPTOR PROTEIN TYROSINE  
 ; TITLE OF INVENTION: PHOSPHATASE INTERACTING PROTEINS  
 ; FILE REFERENCE: 200125, 447  
 ; CURRENT APPLICATION NUMBER: US/10/723,606  
 ; CURRENT FILING DATE: 2003-11-26  
 ; NUMBER OF SEQ ID NOS: 22  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 2  
 ; LENGTH: 1337  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-723-606-2

Query Match 50.4%; Score 878.5; DB 4; Length 1337;  
 Best Local Similarity 56.4%; Pred. No. 1.4e-74;  
 Matches 164; Conservative 56; Mismatches 68; Indels 3; Gaps 3;

QY 18 KTSCPIKINQFESHPKLOADSNLYLSKEYEELKDVGRNOSCDIALLENNNGKRRYNNIL 77  
 DB 1016 KSKSLIRVENFEAYFFKQOADSNGRAEYEDLKVGISQPKYALLENKGRNRNNVL 1075  
 QY 78 PYDATRYVLSNVDDPCSDYINASYIPGNFRREYIVTQGLPGLTKDPFWKRWMEONVAN 137  
 DB 1076 PYDISRVKLS-VQTHSTDDYINANVMPGYHSKQFIATQGLPLENTLKDFMWRWENKRVYA 1134  
 QY 138 IVMVTCQVEKGRKCDHYMPADQPSLYGDLILQMLSESYLPEWTIRREFKICGEQOLDAN 197  
 DB 1133 IIMTKCEVGRKCEYWPSPKQ-AQDYGDIVAMTSEIVLPEWTIRDFYKNIQTSSEH 1193  
 QY 198 RLIRHFHYTWPDHGPVETTSQSLIOFRTVRDYINRSPGAPTVVHCAGVGRGTGFIAL 257  
 DB 1194 PL-RQFHTSMRPHGVPDTDLINFRYLVRDYWKQSPSPSFLVHCAGVGRGTGFIAL 1252  
 QY 258 DRLIQQDSDSDYDIYGAVHDLRLHRVHWVQTECOYVYLHQCVRDVLARK 308  
 DB 1253 DRLIYQIENNTVDYGIYDLRMHRPLMWQTEDOYVFLNQCVDIVASOK 1303

Search completed: February 17, 2006, 01:39:43  
 Job time : 166 secs

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OM protein - protein search, using sw model

Run on: February 17, 2006, 01:37:04, Search time 18 Seconds

(without alignments)  
251,915 Million cell updates/sec

Title: US-10-634-027-7

Perfect score: 1744

Sequence: 1 GRPLSVNLNLCQKGNRKT.....VEDVLRARLKRSEOHNNHH 319

Scoring table:

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Gapop 10.0, Gapext 0.5

Total number of hits satisfying chosen parameters: 107819

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: Published Applications\_AA\_New:  
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8: /cgn2\_6/ptcdat1/pubpaa/US60\_NEW\_PUB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	878.5	50.4	1337	US-11-112-304A-33	Sequence 33, Appl
2	876.5	50.3	1178	US-10-995-861-851	Sequence 851, Appl
3	769	44.0	405	US-11-143-984A-28	Sequence 28, Appl
4	761.5	43.7	1188	US-11-143-984A-27	Sequence 27, Appl
5	697.5	40.0	1711	US-11-143-984A-38	Sequence 38, Appl
6	673.5	38.6	1705	US-11-143-984A-37	Sequence 37, Appl
7	635	36.4	1463	US-11-080-991-22	Sequence 22, Appl
8	618.5	35.5	2314	US-11-097-728-6	Sequence 2, Appl
9	618.5	35.5	2353	US-11-097-728-6	Sequence 2, Appl
10	616.5	35.3	1445	US-11-169-041-181	Sequence 181, Appl
11	610	35.0	1452	US-10-821-234-1102	Sequence 1102, Appl
12	586	33.6	647	US-11-000-463-722	Sequence 722, Appl
13	586	33.6	1897	US-10-821-234-1635	Sequence 1635, Appl
14	583.5	33.5	1254	US-10-528-031-47	Sequence 47, Appl
15	545	31.3	570	US-11-143-984A-10	Sequence 10, Appl
16	513	29.4	415	US-10-444-826-14	Sequence 14, Appl
17	513	29.4	415	US-10-444-826-12	Sequence 12, Appl
18	513	29.4	415	US-11-143-984A-29	Sequence 29, Appl
19	513	29.4	415	US-10-444-826-10	Sequence 10, Appl
20	500	28.9	363	US-10-444-826-8	Sequence 8, Appl
21	496	28.4	339	US-10-509-773-5	Sequence 5, Appl
22	492	28.2	426	US-11-157-489-5	Sequence 5, Appl
23	473.5	27.2	463	US-11-157-489-6	Sequence 6, Appl
24	473.5	27.2	463	US-11-157-489-6	Sequence 6, Appl
25	473.5	27.2	463	US-11-157-489-6	Sequence 6, Appl

26	473	27.1	1267	US-11-109-156-35	Sequence 35, Appl
27	449.5	25.8	405	US-11-197-489-7	Sequence 7, Appl
28	448.5	25.7	398	US-10-509-773-10	Sequence 10, Appl
29	439	25.2	657	US-11-109-156-27	Sequence 27, Appl
30	426	24.4	454	US-11-072-512-2092	Sequence 2092, Appl
31	410.5	23.5	1174	US-10-995-861-697	Sequence 697, Appl
32	409.5	23.5	1303	US-11-143-984A-29	Sequence 29, Appl
33	405.5	23.3	537	US-11-109-156-28	Sequence 28, Appl
34	404.5	23.2	565	US-11-072-512-2180	Sequence 2180, Appl
35	387	22.8	1015	US-11-169-041-217	Sequence 217, Appl
36	387	22.8	1015	US-11-169-041-217	Sequence 217, Appl
37	387	22.8	1015	US-11-169-041-217	Sequence 217, Appl
38	387	22.8	1015	US-11-169-041-217	Sequence 217, Appl
39	387	22.8	1015	US-11-169-041-217	Sequence 217, Appl
40	387	22.8	1015	US-11-169-041-217	Sequence 217, Appl
41	387	22.8	1015	US-11-169-041-217	Sequence 217, Appl
42	387	22.8	1015	US-11-169-041-217	Sequence 217, Appl
43	387	22.8	1015	US-11-169-041-217	Sequence 217, Appl
44	387	22.8	1015	US-11-169-041-217	Sequence 217, Appl
45	387	22.8	1015	US-11-169-041-217	Sequence 217, Appl

## ALIGNMENTS

RESULT 1  
US-11-112-304A-33  
Sequence 33, Application US/11112304A  
Publication No. US2006002931A1  
GENERAL INFORMATION:  
APPLICANT: AMGEN, INC.  
APPLICANT: AMGEN, INC.  
APPLICANT: Smothers, James  
APPLICANT: Farnsworth III, William C.  
APPLICANT: Kaitiv, Revital  
TITLE OF INVENTION: ANTIBODIES OF ANGIOGENESIS INHIBITING DOMAINS OF CD148  
FILE REFERENCE: 3447  
CURRENT APPLICATION NUMBER: US/11/112,304A  
CURRENT FILING DATE: 2005-04-22  
PRIOR APPLICATION NUMBER: US 60/565,158  
PRIOR FILING DATE: 2004-04-23  
PRIOR APPLICATION NUMBER: US 60/564,885  
PRIOR FILING DATE: 2004-04-23  
PRIOR APPLICATION NUMBER: US 60/571,566  
PRIOR FILING DATE: 2004-05-14  
PRIOR APPLICATION NUMBER: US 60/585,686  
PRIOR FILING DATE: 2004-07-06  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO: 33  
LENGTH: 1337  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-112-304A-33  
Query Match 50.4%; Score 878.5; DB 7; Length 1337;  
Best Local Similarity 56.4%; Pred. No. 2.8e-74;  
Matches 164; Conservative 56; Mismatches 68; Indels 3; Gaps 3;  
QY 18 KTSCPIKIQFEGFMQLQADSNVLSKEYEBELKDVGRNOCIDIALPENKRNKYNIT 77  
DB 1016 KKSILIRVFNFAVFKQKQADSNCGFAEVEDLKVGISOPRYAAELAEKRNKYNVVL 1075  
QY 78 PYATVKSINDDPCSDIYINASYIPANNFRREYIVITQGPLPCTKODFKMVMWQNVN 137  
DB 1076 PYDISRVKLS-VQHSITDYINANVMPYSHKDFIATQGPLPTLKDFFRMVWKNYA 1134  
QY 138 IWWTCVSKRVCCHWYADQDSLYGDLIOMLSESIVPEWTIRREPIGCESDLDH 197  
DB 1135 IIMTKVCQGRKTCCEYVPSKQ-NQDYGDITVAAMTSELVPEWTIRDFVKNIGTSESH 1193  
QY 138 RLIRHRYWVMDGCVETQSGLQFVTRDYINSPGAGPTVWCSGVRCTFTAL 257

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Db      1194 PL-ROFHTSWPDHGVPTDITLLINFRYLWDMKQSPSPFLVHCAGVGRGTFFAI 1252
Qy      258 DRILQOLDSKDSVDIYGAVHDLRLHRVHVOTECQYVYLHQCVRDLPRK 308
      1253 DRLIYOIENENTVDYGVIGVYDLRMRPLMVOTEDQYVFLNQCVDIYVSOK 1303

REST 7 2
US-11-995-561-851
; Sequence 851, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE OF INVENTION: DETECTION AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/10/995,561
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 851
; LENGTH: 1178
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-851

Query Match      50.3%; Score: 876.5; DB 6; Length 1178;
Best Local Similarity 56.6%; Pred. No. 3.7e-74;
Matches 162; Conservative 56; Mismatches 65; Indels 3; Gaps 3;

Qy      23 IKINQFGHFMKLOADSNVYLKSEYEELKDVGRNOSCDIALLPENRGHRYNNILPYDAT 82
      862 IRVNFAYFKKQKQADSNCGFAFEYEDLVGISQPKYALFLAENRGHRYNNILPYDIS 921
Db      862 IRVNFAYFKKQKQADSNCGFAFEYEDLVGISQPKYALFLAENRGHRYNNILPYDIS 921
Qy      83 RYKLSNVDDPCSDYINASYPGNNFRREYITOGPLPGTKDPMKMWMEONVANIYVMT 142
      922 RYKLS-VQHSITDDIYNNVWEGHSGKOFITGCPPLTNDPMRWMEKNYAIIMLT 980
Db      143 OCTGKGVKCDHWVADODSLYGDILLQMLSESYLEMTPEFCIEBDLHRLH 202
      981 KCVQGRTKCEELWESKO-ADDTGDIYANISLVEEMTIRFVXKIQSESHP-LRQ 1038
Qy      203 FHYTWPDHGVPTTOSLIQFRTVEDYINNSPGAGFTVYHCSAGVGRGTFFALDRILQ 262
      1039 FHYTWPDHGVPTTDLINFRYLWDMKQSPSPFLVHCAGVGRGTFFALDRILY 1098
Db      1039 FHYTWPDHGVPTTDLINFRYLWDMKQSPSPFLVHCAGVGRGTFFALDRILY 1098
Qy      263 QLDKSDVDIYGAVHDLRLHRVHVOTECQYVYLHQCVRDLPRK 308
      1099 QIENENTVDYGVIGVYDLRMRPLMVOTEDQYVFLNQCVDIYVSOK 1144
Db      1099 QIENENTVDYGVIGVYDLRMRPLMVOTEDQYVFLNQCVDIYVSOK 1144

RESULT 3
US-11-143-984A-28
; Sequence 28, Application US/11143984A
; Publication No. US20060014180A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL HUMAN PHOSPHATASES
; FILE REFERENCE: DD072 DIV1
; CURRENT APPLICATION NUMBER: US/11/143,984A
; PRIOR FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US 60/256,868
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 60/280,186
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/287,735
; PRIOR FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: US 60/295,848
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/300,465
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 208

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; SOFTWARE: Patentin version 3.2
; SEQ ID NO 28
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-143-984A-28

Query Match      44.0%; Score 768; DB 7; Length 405;
Best Local Similarity 48.9%; Pred. No. 1.4e-64;
Matches 149; Conservative 59; Mismatches 87; Indels 10; Gaps 4;

Qy      2 DPLSLVHLNUGKQ--NRKTSCEPKINQFEGHFMKLOADSNVYLKSEYEELKDVGRNOS 58
      83 DYLLAFYINPMSKGLKRRKLTNVOLDPDSYIDWAKSDYKSLQFEELKIGLDIP 142
Db      59 CDIALPENRGHRYNNILPYDATRYVLSNVDDPCSDYINASYPGNNFRREYITOGPL 118
      143 HPAADLPINCKRYNNILPDPFRVRLVSMEEEGADYINANYIPGYNSPOEYIATQCP 202
Qy      119 LGCTDDPMKMWMEONVANIYVMTQCEKGRYKCDHWVADODSLYGDILLQMLSESYL 178
      203 LPTNDPMKMWVLOKSHIYMLQCNKERRKXCDHWVADODSLYGDILLQMLSESYL 262
Qy      179 PEMTIRFKICGEQDLHRLHREHYTWPDHGV--ETTSLOFRTVRYDYNRSPG 236
      263 EDWASRAFR--NVADAQVWHEFNITGPHGVPPANAESILQFVTVRQGAAS-- 317
Db      237 AGFTVYHCSAGVGRGTFFALDRILQOLDSKDSVDIYGAVHDLRLHRVHVOTECQYVYL 296
      318 KSPMTIRHCSAGVGRGTFFALDRILQIRHDEFVLDIGLVSEKRSIRMSVQITEQYIFI 377
Qy      297 HOCVR 301
      378 HOCVO 382
Db      378 HOCVO 382

RESULT 4
US-11-143-984A-27
; Sequence 27, Application US/11143984A
; Publication No. US20060014180A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL HUMAN PHOSPHATASES
; FILE REFERENCE: DD072 DIV1
; CURRENT APPLICATION NUMBER: US/11/143,984A
; PRIOR FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US 60/256,868
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 60/280,186
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/287,735
; PRIOR FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: US 60/295,848
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/300,465
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 27
; LENGTH: 1188
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-11-143-984A-27

Query Match      43.7%; Score 761.5; DB 7; Length 1188;
Best Local Similarity 49.8%; Pred. No. 2.3e-63;
Matches 143; Conservative 56; Mismatches 81; Indels 7; Gaps 3;

Qy      17 RTGSPKINQFEGHFMKLOADSNVYLKSEYEELKDVGRNOSCDIALLPENRGHRYNNI 76
      884 RLTNPVQDLDPAYIKXMAKSDYKSLQFEELKIGLDIPHPAADLPINCKRYNNI 943
Db      77 LPTNDPMKMWVDDPCSDYINASYPGNNFRREYITOGPLPGTKDPMKMWMEONV 136

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Db 944 LPDPSRVALYSWNEEGADYINANVITNSPEEITATOGSLPETHNDPWGMVILQCSQ 1003
137 NIMWTQCEKGRVYKCDHWYPADQSLYYGDLIOMLSVLPMTREKICGSEQLDA 136
1004 IIMLTQCEKGRVYKCDHWYPADQSLYYGDLIOMLSVLPMTREKICGSEQLDA 1060
197 HRLIRHFHTYVDPHGVPE-ETTGSLIOFRTVTDYINRSFGAGPTVVCAGVGTGT 254
1061 MGVWMENTYAMPDHGPTANNAESILQFVHVRQOATKS--KQPMIHCSSAGVGTGT 1118
255 IALDRILQOLDSVDIYGAVHDLRLHRVHMVQTECOYVYLHOCV 301
1119 IALDRILQOLDSVDIYGAVHDLRLHRVHMVQTECOYVYLHOCV 1165

RESULT 5
US-11-143-984A-38
Sequence 38, Application US/11143984A
Publication No. US20060014180A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL HUMAN PHOSPHATASES
FILE REFERENCE: D0072 DIV1
CURRENT APPLICATION NUMBER: US/11/143,984A
PRIOR FILING DATE: 2005-06-02
PRIOR APPLICATION NUMBER: US 60/256,868
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: US 60/280,186
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/287,735
PRIOR FILING DATE: 2001-05-01
PRIOR APPLICATION NUMBER: US 60/295,848
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/300,465
PRIOR FILING DATE: 2001-06-25
NUMBER OF SEQ ID NOS: 208
SOFTWARE: PatentIn version 3.2
SEQ ID NO 38
LENGTH: 1711
TYPE: PRT
ORGANISM: Rattus norvegicus
US-11-143-984A-38

Query Match 40.0%; Score 697.5; DB 7; Length 1711;
Best Local Similarity 46.1%; Pred. No. 3,8e-57;
Matches 131; Conservative 59; Mismatches 91; Indels 3; Gaps 2;

Db 18 KTSCKIKNOPEGHFMKLODSDNYLSKEYEELKDYGNOSCDIALPBRGKRNYYIL 77
1125 KTRHPILPSHRSOSTEKSARHAKQFPQEBELAEVGKQPRLEAHPNIIKRRPHVL 1184
78 PYDATRVKLSNVDDPCSDYINASTYIPGNNFRREYIVTQGPLPGTKDPRKAWMEQVHN 137
1185 PYDSRVRLTQLPQEPHSYDINANFIPGYSHTOEIATOGPLKKTLEDPRWLMEQOVHV 1244
138 IYAVTQCEKGRVYKCDHWYPADQSLYYGDLIOMLSVLPMTREKICGSEQLDA 196
1245 IIMLTQCEKGRVYKCDHWYPADQSLYYGDLIOMLSVLPMTREKICGSEQLDA 1302
197 HRLIRHFHTYVDPHGVPE-ETTGSLIOFRTVTDYINRSFGAGPTVVCAGVGTGT 256
1303 ORRVKQLQFTTWDPHSPVAPESLSLAFVHVOEVATOGKGPLVHCSAGVGTGT 1362
257 LDRILQOLDSVDIYGAVHDLRLHRVHMVQTECOYVYLHOCV 300
1363 LDRILQOLDSVDIYGAVHDLRLHRVHMVQTECOYVYLHOCV 1406

RESULT 6
US-11-143-984A-37
Sequence 37, Application US/11143984A
Publication No. US20060014180A1

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GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL HUMAN PHOSPHATASES
FILE REFERENCE: D0072 DIV1
CURRENT APPLICATION NUMBER: US/11/143,984A
PRIOR FILING DATE: 2005-06-02
PRIOR APPLICATION NUMBER: US 60/256,868
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: US 60/280,186
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/287,735
PRIOR FILING DATE: 2001-05-01
PRIOR APPLICATION NUMBER: US 60/295,848
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/300,465
PRIOR FILING DATE: 2001-06-25
NUMBER OF SEQ ID NOS: 208
SOFTWARE: PatentIn version 3.2
SEQ ID NO 37
LENGTH: 1705
TYPE: PRT
ORGANISM: Mus musculus
US-11-143-984A-37

Query Match 38.6%; Score 673.5; DB 7; Length 1705;
Best Local Similarity 45.1%; Pred. No. 6,9e-55;
Matches 128; Conservative 57; Mismatches 96; Indels 3; Gaps 2;

Db 18 KTSCKIKNOPEGHFMKLODSDNYLSKEYEELKDYGNOSCDIALPBRGKRNYYIL 77
1125 KTRHPILPSHRSOSTEKSARHAKQFPQEBELAEVGKQPRLEAHPNIIKRRPHVL 1184
78 PYDATRVKLSNVDDPCSDYINASTYIPGNNFRREYIVTQGPLPGTKDPRKAWMEQVHN 137
1185 PYDSRVRLTQLPQEPHSYDINANFIPGYSHTOEIATOGPLKKTLEDPRWLMEQOVHV 1244
138 IYAVTQCEKGRVYKCDHWYPADQSLYYGDLIOMLSVLPMTREKICGSEQLDA 196
1245 IIMLTQCEKGRVYKCDHWYPADQSLYYGDLIOMLSVLPMTREKICGSEQLDA 1302
197 HRLIRHFHTYVDPHGVPE-ETTGSLIOFRTVTDYINRSFGAGPTVVCAGVGTGT 256
1303 ORRVKQLQFTTWDPHSPVAPESLSLAFVHVOEVATOGKGPLVHCSAGVGTGT 1362
257 LDRILQOLDSVDIYGAVHDLRLHRVHMVQTECOYVYLHOCV 300
1363 LDRILQOLDSVDIYGAVHDLRLHRVHMVQTECOYVYLHOCV 1406

RESULT 7
US-11-080-991-22
Sequence 22, Application US/11080991
Publication No. US20050266437A1
GENERAL INFORMATION:
APPLICANT: Velby, Peter Ole
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST TUMORS
FILE REFERENCE: MRI-039
CURRENT APPLICATION NUMBER: US/11/080,991
PRIOR FILING DATE: 2005-03-11
PRIOR APPLICATION NUMBER: US/10/176,847
PRIOR FILING DATE: 2002-06-21
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 22
LENGTH: 1463
TYPE: PRT
ORGANISM: Homo sapiens
US-11-080-991-22

Query Match 36.4%; Score 635; DB 7; Length 1463;
Best Local Similarity 46.4%; Pred. No. 2,3e-51;

```



Matches 130; Conservative 47; Mismatches 93; Indels 10; Gaps 6;

QY 23 IKINQFBSHFMKQADSNYLKSEYEELKDVGRN-OSCDIAL-----LPENRGKRY 73  
 DB 891 IRVADLQHTOMKQCGKREYELPE-QQTSMTAKENENKRRGINISYDS 949  
 QY 83 RYKLSNDPDCSDYNASYPGNPFREYITQGLPGKDFPMWMEONVIMWT 142  
 DB 950 RYKLVLDSPHSDYNNANIDGHRPHYITQPMQETVKDFPMIWMNSASIMWT 1009  
 QY 143 QCVKGRKCDHWPPADDSLYGDLILMLSESLPEMTIREFKICEBOLDH--RLI 200  
 DB 1010 NIVEGRKCVRWPDTE--YGDIKVTLITREBLAIVIRFTV--QKGYHEREL 1064  
 QY 201 RHFTYTPHGVPEETOSLIQVRYTRDYINRSFGAFVTVHCSGGRGTIALDI 260  
 DB 1065 RLHFTSPHGVPCYATGELGAFYQVK-FLN-PEAGPVIWCSGAGRTCFIALDI 1122  
 QY 261 LQOLDSKSDYIYGAVDLRLHRYVMQTECOYVYLHCY 300  
 DB 1123 LDMENEGVDIFNCVREIRAEQVNLVQTEBOYVFHDAI 1162

RESULT 8  
 US-11-097-728-2  
 / Sequence 2, Application US/11097728  
 / Publication No. US20050260132A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Sabine Muller  
 / APPLICANT: Daniel J. Chin  
 / APPLICANT: Mirilla Gonzalez-Zulueta  
 / TITLE OF INVENTION: MONOCLONAL ANTIBODIES DIRECTED TO RECEPTOR PROTEIN  
 / TITLE OF INVENTION: TYROSINE PHOSPHATASE ZETA  
 / FILE REFERENCE: AGT-006CIP  
 / CURRENT APPLICATION NUMBER: US/11/097,728  
 / PRIOR FILING DATE: 2005-03-31  
 / PRIOR APPLICATION NUMBER: 10/652,981  
 / NUMBER OF SEQ ID NOS: 14  
 / SOFTWARE: FASTSEQ for Windows Version 4.0  
 / SEQ ID NO 2  
 / LENGTH: 2314  
 / TYPE: PRT  
 / ORGANISM: Homo Sapiens  
 / US-11-097-728-2

Query Match 35.5%; Score 618.5; DB 7; Length 2314;  
 Best Local Similarity 42.2%; Pred. No. 1.5e-49;  
 Matches 132; Conservative 54; Mismatches 104; Indels 23; Gaps 8;

QY 23 IKINQFBSHFMKQADSNYLKSEYEELKDVGRN-OSCDIAL-----LPENRGKRY 73  
 DB 1698 IPIKHPFHVADLHASSGF--TEFETLKEFQEVQSCVLDGITADSSNHPDKHKNRY 1755  
 QY 74 NNLIPYDTRYKLSNV--DDPCSDYNASYPGNPFREYITQGLPGKDFPMWMEONVIMWT 131  
 DB 1756 INIVAYDSRKYLAQLAEKDGLTDYNNANIDGHRPHYITQPMQETVKDFPMIWMNSASIMWT 1815  
 QY 132 EQNVNITVMTQCVKGRKCDHWPPADDSLYGDLILMLSESLPEMTIREF----- 186  
 DB 1816 ENHVEVYIMTNLVEGRKRCQWMPAD--GSEBYGNFLVQKSVQVLAVYVIRNFTLRNT 1874  
 QY 187 --KICEBOLDARLRLHFTYTPHGVPEETOSLIQVRYTRDYINRSFGAFVTVH 244  
 DB 1875 KIKKSGQGRPSGRVVTQYHTQWPDWGVPEISLVLTFAKXA--YAKH-AVGPVYVHC 1932  
 QY 245 SAGVGRGTGTIALDRLIQOLDSKSDYIYGAVDLRLHRYVMQTECOYVYLHCY 304  
 DB 1933 SAGVGRGTGTIYVDSMLQOIQHEGTVINIFGLKHIRSQRNVLVQTEBOYVFHDTLVEAI 1992

QY 305 PARKLRSEQHNNH 317  
 DB 1992 LSKETEVLDSDIH 2005

DB 1993 LSKETEVLDSDIH 2005

RESULT 9  
 US-11-097-728-6  
 / Sequence 6, Application US/11097728  
 / Publication No. US20050260132A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Erik Poeht  
 / APPLICANT: Sabine Muller  
 / APPLICANT: Daniel J. Chin  
 / APPLICANT: Mirilla Gonzalez-Zulueta  
 / TITLE OF INVENTION: MONOCLONAL ANTIBODIES DIRECTED TO RECEPTOR PROTEIN  
 / TITLE OF INVENTION: TYROSINE PHOSPHATASE ZETA  
 / FILE REFERENCE: AGT-006CIP  
 / CURRENT APPLICATION NUMBER: US/11/097,728  
 / PRIOR FILING DATE: 2005-03-31  
 / PRIOR APPLICATION NUMBER: 10/652,981  
 / NUMBER OF SEQ ID NOS: 14  
 / SOFTWARE: FASTSEQ for Windows Version 4.0  
 / SEQ ID NO 6  
 / LENGTH: 2353  
 / TYPE: PRT  
 / ORGANISM: Homo sapiens  
 / FEATURE:  
 / NAME/KEY: VARSPLIC  
 / LOCATION: (1)...(2353)  
 / OTHER INFORMATION: PTP-zeta SM2 23a exon variant  
 / US-11-097-728-6

Query Match 35.5%; Score 618.5; DB 7; Length 2353;  
 Best Local Similarity 42.2%; Pred. No. 1.5e-49;  
 Matches 133; Conservative 54; Mismatches 104; Indels 23; Gaps 8;

QY 23 IKINQFBSHFMKQADSNYLKSEYEELKDVGRN-OSCDIAL-----LPENRGKRY 73  
 DB 1698 IPIKHPFHVADLHASSGF--TEFETLKEFQEVQSCVLDGITADSSNHPDKHKNRY 1755  
 QY 74 NNLIPYDTRYKLSNV--DDPCSDYNASYPGNPFREYITQGLPGKDFPMWMEONVIMWT 131  
 DB 1756 INIVAYDSRKYLAQLAEKDGLTDYNNANIDGHRPHYITQPMQETVKDFPMIWMNSASIMWT 1815  
 QY 132 EQNVNITVMTQCVKGRKCDHWPPADDSLYGDLILMLSESLPEMTIREF----- 186  
 DB 1816 ENHVEVYIMTNLVEGRKRCQWMPAD--GSEBYGNFLVQKSVQVLAVYVIRNFTLRNT 1874  
 QY 187 --KICEBOLDARLRLHFTYTPHGVPEETOSLIQVRYTRDYINRSFGAFVTVH 244  
 DB 1875 KIKKSGQGRPSGRVVTQYHTQWPDWGVPEISLVLTFAKXA--YAKH-AVGPVYVHC 1932  
 QY 245 SAGVGRGTGTIALDRLIQOLDSKSDYIYGAVDLRLHRYVMQTECOYVYLHCY 304  
 DB 1933 SAGVGRGTGTIYVDSMLQOIQHEGTVINIFGLKHIRSQRNVLVQTEBOYVFHDTLVEAI 1992

QY 305 PARKLRSEQHNNH 317  
 DB 1993 LSKETEVLDSDIH 2005

RESULT 10  
 US-11-169-041-181  
 / Sequence 181, Application US/11169041  
 / Publication No. US20060019284A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Bristol-Myers Squibb Company  
 / TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF  
 / TITLE OF INVENTION: COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE  
 / TITLE OF INVENTION: KINASES AND/OR PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANCER  
 / FILE REFERENCE: 10001 NP  
 / CURRENT APPLICATION NUMBER: US/11/169,041  
 / PRIOR FILING DATE: 2005-06-28

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; PRIOR APPLICATION NUMBER: 60/584,405
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 527
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 181
; LENGTH: 1445
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-169-041-181

Query Match      35.3%; Score 616.5; DB 7; Length 1445;
Best Local Similarity 37.8%; Pred. No. 1.2e-49;
Matches 133; Conservative 64; Mismatches 106; Indels 49; Gaps 8;

QY 12 GQKMK-----TSCP-----IKINQEGHFMKLOADSNY 41
DB 787 GEGSKPKGOTAHFYVDSSSPRVVPNESPPIPIPDWENAI PKQGVHIGELYSNNOH 846
QY 42 LSKKEYELK--DVGKQSCDIALLPENRGNKNNILPYDATEVKLSNV--DDPPGSDY 97
DB 847 GFSEDFEEVORCTADNMTAESHNNPEKKNRYINILAYDSHVKLRLPKGKSKSDY 906
QY 98 INASYIPGNFRREYIVTQGLPGTKDFPMQWMEQVNIWMTQCVKEKGVKCDHYMP 157
DB 907 INANVYDGNKAKAYIATQGLPKSTFEDFWRMTWENQGIIVMTNLVKGRRKCDQYWE 966
QY 158 ADDDSLYTGDDILQMLSESVLPMTIREPKICEEQDLA-----HRLHRYHYTV 207
DB 967 T-ENSEKGNITVLTSTKIHCTYRFSIRTKYKGGKGNPKGRKMERVYVQHYHQ 1025
QY 208 WPHQVPEPTOSLQPRVRYIRNSGAGPVVHCNSGGRGTFFILDLQGLDGR 267
DB 1026 WPMKGPPEALPVLTFR--KSSANRPETGPVLVHCNSGAGRGITVYIDMLQIKDK 1083
QY 268 DSDYIYGAHDLRLHRYVMTQECQYVYLHCVRDYL--RAKRLSEQHNN 317
DB 1084 STVNVLGFLKRIORTORNYLVQTEBOYIPIHDALLKIKETEVSSNOLASY 1135

RESULT 11
US-10-821-234-1102
; Sequence 1102, Application US/10821234
; Publication No. US2005025514A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Brigitte
; APPLICANT: Andarmanj, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; PRIOR FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: PC_Seq_genes Version 1.0
; SEQ ID NO 1102
; LENGTH: 1452
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1102

Query Match      35.0%; Score 610; DB 6; Length 1452;
Best Local Similarity 44.6%; Pred. No. 5.1e-49;
Matches 125; Conservative 42; Mismatches 103; Indels 10; Gaps 5;

QY 23 IKINQEGHFMKLOADSNYLSKEYEELKDVGRNOSCDIALLPENRGNKNNILPYDAT 82
DB 880 IRVADLQHTQKCKAGYGFKEYESFEF--QSAFPMWDSAKDENNMORRYGNIAVDHS 936
QY 83 RYKSNVDDPCSDYINASYIPGNFRREYIVTQGLPGTKDFPMQWMEQVNIWMT 142
DB 939 RYLOTEGTSNDYINSGYIDGHRPNHYIATQGMETIYDFRMWMENTASTIMVT 998

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QY 143 QCVKEKGVKCDHYMPADODSLYYGDLIQLMLSESVLPMTIREPKICEEQDLA--RLI 200
DB 999 NLVEGRVKCKYMPDDTE--YKDIKVTLLIETELLAYVIRTFV--EKGVHEIRI 1053
QY 201 RHFYTWPDHGVPEPTOSLQPRVRYIRNSGAGPVVHCNSGGRGTFFIALRLI 260
DB 1054 RQHFITQMDHGVFPHATGLGTYVQVKS--KSPFSAGPLVYHCSAAGRTGTFIVDIM 1111
QY 261 LQGLDSDSDYDYGAHDLRLHRYVMTQECQYVYLHCVR 300
DB 1112 LDMALRGVVDIYNCKVELHSRRVNVQTEBOYVFIHDNI 1151

RESULT 12
US-11-000-463-722
; Sequence 722, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Dmanac, Radolje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785C1PACN
; CURRENT APPLICATION NUMBER: US/11/000,463
; PRIOR FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: RastSeq for Windows Version 3.0
; SEQ ID NO 722
; LENGTH: 647
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-722

Query Match      33.6%; Score 586; DB 7; Length 647;
Best Local Similarity 42.6%; Pred. No. 3.1e-47;
Matches 127; Conservative 52; Mismatches 101; Indels 18; Gaps 7;

QY 22 PIKINQEGHFMKLOADSNYLSKEYEELKDVGRNOSCDIALLPENRGNKNNILPYDA 81
DB 71 PIPTDLADNTERKKNADLKFQSEYESI--DPQOFTWENSLEVKPRGRYANVIAVDH 129
QY 82 TRYKSNVDDPCSDYINASYIPGNFRREYIVTQGLPGTKDFPMQWMEQVNIWMT 141
DB 130 SRVYILTSIDVPGSDYINANVYIDYRKONAYIATQGLPEPTMGDFWRMWMEQRTATVVM 189
QY 142 TVCVKEKGVKCDHYMPADODSLYYGDLIQLMLSESVLPMTIREPKICEEQDLAHL 199
DB 190 TRLEKSNVKKDDQWPA--RGTEGGLQVTLDTVELATVTRTFALHKSGSSE--KRE 245
QY 200 IRHFHYTWPDHGVPEPTOSLQPRVRYIRNSG--GAGPYVHCSAGVKTGTFIALD 258

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DB 246 LRQGFPMAMDHGVPEYPTPLATLARKVAC---NPLDAGPMVHCASGVRTGCFIVD 302  
 QY 259 RILQOOLDSKSDYICAVHDLRLHRVAMQTECOVYVILHO-----CYRDVLRARL 309  
 DB 303 AMLEBMKHEKTVIYGHVTCMRSGRNVMQTEDQVYFIHEALLLEAATGHTVEVPAEML 360

RESULT 13  
 US-10-821-234-1635  
 / Sequence 1635, Application US/10821234  
 / Publication No. US20050255114A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Labat, Ivan  
 / APPLICANT: Stache-Crain, Bitgit  
 / APPLICANT: Andarmani, Susan  
 / APPLICANT: Tang, Y. Tom  
 / TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
 / FILE REFERENCE: 821A  
 / CURRENT APPLICATION NUMBER: US/10/821,234  
 / CURRENT FILING DATE: 2004-04-07  
 / PRIOR APPLICATION NUMBER: US 60/462,047  
 / PRIOR FILING DATE: 2003-04-07  
 / NUMBER OF SEQ ID NOS: 1704  
 / SOFTWARE: pt seq\_genes version 1.0  
 / SEQ ID NO: 1635  
 / LENGTH: 1897  
 / TYPE: PRT  
 / ORGANISM: Homo sapiens  
 US-10-821-234-1635

Query Match 33.6%; Score 586; DB 6; Length 1897;

Best Local Similarity 42.6%; Pred. No. 1.3e-46;  
 Matches 127; Conservative 52; Mismatches 101; Indels 18; Gaps 7;

QY 22 PIKINQFEGHFMKLQADSNVYLSKEYELKDVGRNOSCDIALPENRGKRNINILPYDA 81  
 DB 1331 PIPITDLADNIEBRLKANDGLKFSQSEYESI-DGQOFTWENSLEVKRKNYANVAYADH 1379  
 QY 82 TRVKSANVDDPCSDYINASYIPGNRRREYIVTGGPLPCTKDEFKWMEONVHINIVV 141  
 DB 1380 SSVILTSIDVPGSDVINANYIDYRKONAYIATGGPLPETMGDFWRWVMEORATATVVM 1439  
 QY 142 TCQVKGRCVCHWYPADQDSLYGDLILQMLSESVLPWTIREFKI--CGEOLDARL 199  
 DB 1440 TRLEKSRVACDQYMA-RGTETGGLQVTLDTVELATYVTRTFALHKSSE--KRE 1495  
 QY 200 IRHFHYVWDPHGVPTTOSLIQFRTVDYINRSP-GAGPTVHCSAGVGTGTFIAD 258  
 DB 1496 LRQGFPMAMDHGVPEYPTPLATLARKVAC---NPLDAGPMVHCASGVRTGCFIVD 1552  
 QY 259 RILQOOLDSKSDYICAVHDLRLHRVAMQTECOVYVILHO-----CYRDVLRARL 309  
 DB 1553 AMLEBMKHEKTVIYGHVTCMRSGRNVMQTEDQVYFIHEALLLEAATGHTVEVPAEML 1610

RESULT 14  
 US-11-000-463-250  
 / Sequence 250, Application US/11000463  
 / Publication No. US2005026423A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Tang, Y. Tom  
 / APPLICANT: Liu, Chenghua  
 / APPLICANT: Asundi, Vinod  
 / APPLICANT: Chen, Rui-hong  
 / APPLICANT: Qian, Xiaohong B.  
 / APPLICANT: Wang, Zhiwei  
 / APPLICANT: Wehman, Tom  
 / APPLICANT: Zhou, Ping  
 / APPLICANT: Cao, Yi-cheng  
 / APPLICANT: Drmanac, Radoje T.  
 / TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides

FILE REFERENCE: 785CIP4CN  
 / CURRENT APPLICATION NUMBER: US/11/000,463  
 / CURRENT FILING DATE: 2004-11-29  
 / PRIOR APPLICATION NUMBER: 10/291,265  
 / PRIOR FILING DATE: 2002-11-08  
 / PRIOR APPLICATION NUMBER: PCT/US01/02623  
 / PRIOR FILING DATE: 2001-01-25  
 / PRIOR APPLICATION NUMBER: 09/922,279  
 / PRIOR FILING DATE: 2001-08-03  
 / PRIOR APPLICATION NUMBER: 09/491,404  
 / PRIOR FILING DATE: 2000-01-25  
 / PRIOR APPLICATION NUMBER: 09/617,746  
 / PRIOR FILING DATE: 2000-07-17  
 / PRIOR APPLICATION NUMBER: 09/631,451  
 / PRIOR FILING DATE: 2000-08-03  
 / PRIOR APPLICATION NUMBER: 09/633,870  
 / PRIOR FILING DATE: 2000-09-15  
 / NUMBER OF SEQ ID NOS: 944  
 / SOFTWARE: FastSeq for Windows version 3.0  
 / SEQ ID NO: 250  
 / LENGTH: 1907  
 / TYPE: PRT  
 / ORGANISM: Homo sapiens  
 US-11-000-463-250

Query Match 33.6%; Score 586; DB 7; Length 1907;

Best Local Similarity 42.6%; Pred. No. 1.3e-46;  
 Matches 127; Conservative 52; Mismatches 101; Indels 18; Gaps 7;

QY 22 PIKINQFEGHFMKLQADSNVYLSKEYELKDVGRNOSCDIALPENRGKRNINILPYDA 81  
 DB 1331 PIPITDLADNIEBRLKANDGLKFSQSEYESI-DGQOFTWENSLEVKRKNYANVAYADH 1389  
 QY 82 TRVKSANVDDPCSDYINASYIPGNRRREYIVTGGPLPCTKDEFKWMEONVHINIVV 141  
 DB 1390 SSVILTSIDVPGSDVINANYIDYRKONAYIATGGPLPETMGDFWRWVMEORATATVVM 1449  
 QY 142 TCQVKGRCVCHWYPADQDSLYGDLILQMLSESVLPWTIREFKI--CGEOLDARL 199  
 DB 1450 TRLEKSRVACDQYMA-RGTETGGLQVTLDTVELATYVTRTFALHKSSE--KRE 1505  
 QY 200 IRHFHYVWDPHGVPTTOSLIQFRTVDYINRSP-GAGPTVHCSAGVGTGTFIAD 258  
 DB 1506 LRQGFPMAMDHGVPEYPTPLATLARKVAC---NPLDAGPMVHCASGVRTGCFIVD 1562  
 QY 259 RILQOOLDSKSDYICAVHDLRLHRVAMQTECOVYVILHO-----CYRDVLRARL 309  
 DB 1563 AMLEBMKHEKTVIYGHVTCMRSGRNVMQTEDQVYFIHEALLLEAATGHTVEVPAEML 1620

RESULT 15  
 US-10-528-031-47  
 / Sequence 47, Application US/10528031  
 / Publication No. US2005026257A1  
 / GENERAL INFORMATION:  
 / APPLICANT: ORDIS BIOMED Forschungs- und Entwicklungs GmbH  
 / APPLICANT: Quelly, Christian  
 / APPLICANT: Buck, Charles R.  
 / APPLICANT: Zatloukal, Kurt  
 / TITLE OF INVENTION: Polypeptides and nucleic acids encoding these and their use for  
 / FILE REFERENCE: Oridis Biomed  
 / CURRENT APPLICATION NUMBER: US/10/528,031  
 / CURRENT FILING DATE: 2005-03-16  
 / NUMBER OF SEQ ID NOS: 73  
 / SOFTWARE: Patent version 3.1  
 / SEQ ID NO: 47  
 / LENGTH: 1254  
 / TYPE: PRT  
 / ORGANISM: Mus musculus  
 US-10-528-031-47

Query Match 33.5%; Score 583.5; DB 6; Length 1254;

Best Local Similarity 41.74; Pred. No. 1.3e-46;  
 Matches 118; Conservative 56; Mismatches 104; Indels 5; Gaps 4;

Qy	22	PIKINQFEGHFMKIQADSNYLSKEYEELKDVGNOSCDIALPENRGKRRYNNILPYDA	81
Db	678	PIPIELADHIERLKANDNLKFSQETESI-DPGQFTWEHSNLEVNKPKRRYANVIAYDH	736
Qy	82	TRVYLSNVDDPCSDYINASYIPKNNFRREYIVTQGPLPGTMDPFMGMWQNVNHYMV	141
Db	737	SRVLSAIEGIFGSDYNNAYIDGRKKNAYIATQSLPETGDFMRNWEQRSATVMM	796
Qy	142	TQCVKGRYKCDHWTPADQSLYGDLLQMLSESVLPMTIREFKICGHEQLDHLIR	201
Db	797	TKLEERSKRVKCDYTPS-RGTEHGLVOVTLDTVELATYCVRTFALY-KNGSSEKREVR	854
Qy	202	HFHYVWPDHGVPEPTQSLIQVRYVADYINRSFGAGPTVHCSAGVGTGTFTALDRIL	261
Db	855	QFOFTAMPDHPGVPHPTPLAFIRRYKTC--NPEDAGPMVWHCSAGVGTGCFIVIDAML	912
Qy	262	QQLDSKDSYDIYGAVHDLRLHRYHNVQTECOYVYLHCVRDVL	304
Db	913	ERIKHEKTVDIYGHVTLMRQRRNVVQTEDOYTFIHDLLEAV	955

Search completed: February 17, 2006, 01:40:06  
 Job time : 19 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: February 17, 2006, 01:17:39 / Search time 186 Seconds  
(without alignments)  
753.558 Million cell updates/sec

Title: US-10-634-027-7  
Perfect score: 1744  
Sequence: 1 GDRPLSVHLNIGQKGNKRTS.....VRDVLARKLNSEQHNNH 319

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: A\_Geneseq\_21:\*

1: geneseqp19808:.\*  
2: geneseqp19808:.\*  
3: geneseqp20008:.\*  
4: geneseqp20008:.\*  
5: geneseqp20028:.\*  
6: geneseqp20038:.\*  
7: geneseqp20038:.\*  
8: geneseqp20048:.\*  
9: geneseqp20058:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1744	100.0	319	8	AD004585 Human HPT
2	1691	97.0	336	8	AD004582 Human HPT
3	1691	97.0	1987	3	ABR19774 Human pro
4	1691	97.0	1987	4	AAW78821 Human pro
5	1691	97.0	1987	5	AAE20278 Human PTF
6	1691	97.0	1987	7	ABR57179 Human PTF
7	1691	97.0	1987	7	ADJ70329 Human HPT
8	1691	97.0	2002	8	AD004580 Human HPT
9	1691	97.0	2002	8	AD004584 Human HPT
10	1691	97.0	1450	7	ABR57182 Human PTP
11	1650	94.6	1998	7	AAO24268 Human PTP
12	1650	94.6	1998	7	AAO24268 Human PTP
13	1644	94.3	579	3	AAH19773 Mouse vas
14	1644	94.3	579	3	AAH19773 Mouse vas
15	1367	78.8	310	4	AAH59377 Human PTP
16	878.5	50.4	341	8	ADP74604 Human pro
17	878.5	50.4	1337	2	AAH5203 hndp-1.
18	878.5	50.4	1337	7	AD116193 Human pro
19	878.5	50.4	1337	8	AD116193 Human pro
20	878.5	50.4	1337	8	ADP74603 Amino aci
21	878.5	50.4	1337	9	ADP74603 Amino aci
22	878.5	50.4	1337	9	ADP74603 Amino aci
23	878.5	50.4	1337	9	ADP74603 Amino aci
24	869.5	49.6	1216	7	AD116200 Rat prote

25	868.5	49.8	1238	7	AD116198 Mouse pro
26	850.5	48.8	1647	4	ABR58428 Drosophi
27	829.5	47.6	1767	4	ABR58428 Drosophi
28	805.5	46.2	1447	7	ABR57181 Drosophi
29	775	44.4	1216	2	AAW10685 Human tyr
30	768	44.0	405	5	ABR52339 Protein i
31	768	44.0	405	5	ABR52339 Protein i
32	767	44.0	1217	7	ADP46195 Rat prote
33	767	44.0	1217	7	ADP46195 Rat prote
34	765	43.9	1216	8	ADP46195 Rat prote
35	765	43.9	1216	8	ADP46195 Rat prote
36	764	43.8	405	2	ABR5473 Rabbit os
37	761.5	43.7	378	7	ADP46197 Human pro
38	761.5	43.7	1188	2	ABR52338 Human pro
39	761.5	43.7	1188	5	ABR52338 Human pro
40	761.5	43.7	1188	5	ABR52338 Human pro
41	761.5	43.7	1188	5	ABR52338 Human pro
42	760.5	43.6	1187	8	ADP46195 Rat prote
43	760.5	43.6	1187	8	ADP46195 Rat prote
44	744.5	42.7	309	4	AAW78276 Human aci
45	737.5	42.3	251	4	AAW78276 Human aci

## ALIGNMENTS

## RESULT 1

AD004585 standard; protein; 319 AA.

AD004585;

15-JUL-2004 (first entry)

Human HPTbeta catalytic domain.

Protein co-ordinate data: HPTbeta, HPT-beta, PRPB, PRPBeta; PRPB; R-PTP-beta; angiotensin mediated disorder; diabetic retinopathy; sickle cell anaemia; Paget's disease; mycobacterial infection; systemic lupus erythematosus; myopia; Crohn's disease; psoriasis; rheumatoid arthritis; tumour; acquired immune deficiency syndrome; AIDS; drug desigain; therapy; human.

Homo sapiens.

US2004077065-A1.

22-APR-2004.

04-AUG-2003; 2003US-00634027.

25-SEP-2002; 2002US-0413547P

(PROC) PROCTER & GAMBLE CO.

Evdokimov AG, Pokrosov ME;

WPI; 2004-374235/35.

Identification of compound useful for treatment of angiogenesis mediated disorder, by using three-dimensional structure of HPTbeta catalytic domain, and employing structure to design, or select compound that binds HPTbeta in silico.

Example; SEQ ID NO 7; 315PP; English.

The invention relates to the three dimensional coordinates of HPTbeta (also known as HPT-beta, PRPB, PRPBeta, PTPB or R-PTP-beta) protein. It also relates to a method for the identification of a compound useful for the treatment of an angiogenesis mediated disorder. The compound identified by this method are useful to treat diseases like diabetic retinopathy, sickle cell anaemia, Paget's disease, mycobacterial infections, systemic lupus erythematosus, myopia, Crohn's disease,

PD 25-OCT-2000.  
 XX 23-APR-1999; 99EP-00108074.  
 XX 23-APR-1999; 99EP-00108074.  
 XX (PLAC) MAX PLANCK GES FORDERUNG WISSENSCHAFTEN.  
 XX Fachinger G, Rissau B, Deutsche U;  
 XX WPI; 2000-648832/63.  
 XX N-PSDB; AAK88866.  
 XX Monitoring or modulating Tie-2 tyrosine kinase activity, useful e.g. for  
 XX regulating tumor growth, using vascular-endothelial protein tyrosine  
 XX phosphatase.  
 XX Disclosure; Page 21-27; 60pp; English.  
 XX The present sequence is that of human protein tyrosine phosphatase HPRP-  
 XX beta, a member of subclases III receptor type PTPs, bearing fibronectin  
 XX type III-like repeats in the extracellular domain and a single catalytic  
 XX domain in the cytoplasmic tail. HPRP-beta is a vascular-endothelial  
 XX protein tyrosine phosphatase (VE-PTP) that specifically interacts with  
 XX receptor-tyrosine kinase Tie-2, modulating its tyrosine  
 XX phosphorylation. Tie-2 is involved in angiogenic processes, the  
 XX formation of blood vessels during embryonal development, wound healing  
 XX and in pathological processes such as tumour development. VE-PTPs such as  
 XX HPRP-beta or its catalytic domain, nucleic acids and ligands can be used  
 XX to monitor, stimulate or repress Tie-2 activity for the purposes of  
 XX monitoring or modulating angiogenesis, inducing or inhibiting vascular  
 XX growth or remodeling and blood vessel maturation, and inhibiting tumour  
 XX growth or metastasis  
 XX Sequence 1997 AA;  
 XX  
 XX Query Match 97.0%; Score 1691; DB 3; Length 1997;  
 XX Best Local Similarity 99.4%; Pred. No. 5,6e-179;  
 XX Matches 312; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 OY 2 DRPLSVHLNIGQGNKRTSCPIKINQPEGFHFKLQADSNYLSKEYEELKQVGNOSCDI 61  
 DB 1662 DRPLSVHLNIGQGNKRTSCPIKINQPEGFHFKLQADSNYLSKEYEELKQVGNOSCDI 1721  
 OY 62 ALPENRGNKRYNNILPYDARTVRLSNVDDPCSDYINASYIPGNFRREYIVTQGLPG 121  
 DB 1722 ALPENRGNKRYNNILPYDARTVRLSNVDDPCSDYINASYIPGNFRREYIVTQGLPG 1781  
 OY 122 TKODFMKQWQVNHVWVTCVEKGRVYKCHWYPADODSLYYGDLILQMLSSVLPFW 181  
 DB 1782 TKODFMKQWQVNHVWVTCVEKGRVYKCHWYPADODSLYYGDLILQMLSSVLPFW 1841  
 OY 182 TIREFKICGEQDARLIRHHTVWPDHGVPTTOSLIQFRTVRYINRSPGAPTV 241  
 DB 1842 TIREFKICGEQDARLIRHHTVWPDHGVPTTOSLIQFRTVRYINRSPGAPTV 1901  
 OY 242 VHCAGVGRGTGFIADRIILQOLDSKDSVDIYGVAVHDLRLHVRVWQTECOYVYLHCVR 301  
 DB 1902 VHCAGVGRGTGFIADRIILQOLDSKDSVDIYGVAVHDLRLHVRVWQTECOYVYLHCVR 1961  
 OY 302 DVLRRKLRSEQH 315  
 DB 1962 DVLRRKLRSEQH 1975  
 XX  
 XX RESULT 4  
 XX AAM78821  
 XX ID AAM78821 standard; protein; 1997 AA.  
 XX AC AAM78821;  
 XX XX 06-NOV-2001 (first entry)

DE Human protein SEQ ID NO 1483.  
 XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
 XX vaccine; peptide therapy; stem cell growth factor; hematopoiesis;  
 XX tissue growth factor; immunomodulatory; cancer; leukemia;  
 XX nervous system disorder; arthritis; inflammation.  
 XX Homo sapiens.  
 XX MO200157190-A2.  
 XX 09-AUG-2001.  
 XX 05-FEB-2001; 2001MO-US004098.  
 XX 03-FEB-2000; 2000US-00496914.  
 XX 27-APR-2000; 2000US-00560875.  
 XX 20-UN-2000; 2000US-00560875.  
 XX 19-UN-2000; 2000US-00620325.  
 XX 01-SEP-2000; 2000US-00654936.  
 XX 15-SEP-2000; 2000US-00654936.  
 XX 20-OCT-2000; 2000US-00693325.  
 XX 30-NOV-2000; 2000US-00728422.  
 XX (HYSB-) HYSBQ INC.  
 XX Tang Y, Liu C, Dimaac R, Asundi V, Zhou P, Xu C, Cao Y,  
 XX Ma Y, Zhao Q, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW,  
 XX Xue AJ, Yang Y, Wejhrman T, Goodrich R;  
 XX WPI; 2001-476283/51.  
 XX N-PSDB; AAK51954.  
 XX Nucleic acids encoding polypeptides with cytokine-like activities, useful  
 XX in diagnosis and gene therapy.  
 XX Claim 20; Page 3761-3764; 622pp; English.  
 XX The invention relates to polynucleotides (AAK51456-AAK53435) and the  
 XX encoded polypeptides (AAM78123-AA80302) that exhibit activity relating to  
 XX cytokine, cell proliferation or cell differentiation or which may induce  
 XX production of other cytokines in other cell populations. The  
 XX polynucleotides and polypeptides are useful in gene therapy, vaccines or  
 XX peptide therapy. The polypeptides have various cytokine-like activities,  
 XX e.g. stem cell growth factor activity, hematopoiesis regulating  
 XX activity, tissue growth factor activity, immunomodulatory activity and  
 XX activity/inhibit activity and may be useful in the diagnosis and/or  
 XX treatment of cancer, leukemia, nervous system disorders, arthritis and  
 XX inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111  
 XX (AAK52582) and 3666 (AAM80920) are omitted as the relevant pages from the  
 XX sequence listing were missing at the time of publication  
 XX Sequence 1997 AA;  
 XX  
 XX Query Match 97.0%; Score 1691; DB 4; Length 1997;  
 XX Best Local Similarity 99.4%; Pred. No. 5,6e-179;  
 XX Matches 312; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 OY 2 DRPLSVHLNIGQGNKRTSCPIKINQPEGFHFKLQADSNYLSKEYEELKQVGNOSCDI 61  
 DB 1662 DRPLSVHLNIGQGNKRTSCPIKINQPEGFHFKLQADSNYLSKEYEELKQVGNOSCDI 1721  
 OY 62 ALPENRGNKRYNNILPYDARTVRLSNVDDPCSDYINASYIPGNFRREYIVTQGLPG 121  
 DB 1722 ALPENRGNKRYNNILPYDARTVRLSNVDDPCSDYINASYIPGNFRREYIVTQGLPG 1781  
 OY 122 TKODFMKQWQVNHVWVTCVEKGRVYKCHWYPADODSLYYGDLILQMLSSVLPFW 181  
 DB 1782 TKODFMKQWQVNHVWVTCVEKGRVYKCHWYPADODSLYYGDLILQMLSSVLPFW 1841  
 OY 182 TIREFKICGEQDARLIRHHTVWPDHGVPTTOSLIQFRTVRYINRSPGAPTV 241  
 DB 1842 TIREFKICGEQDARLIRHHTVWPDHGVPTTOSLIQFRTVRYINRSPGAPTV 1901

immunomodulator; gene therapy; metabolic disease; eating disorder;  
 body weight regulation disorder; cachexia; diabetes mellitus; cancer;  
 hypertension; coronary heart disease; hypercholesterolaemia; gallstone;  
 dyslipidaemia; osteoarthritis; sleep apnea; human; chromosome 12;  
 protein tyrosine phosphatase receptor type B precursor; PTPRB.  
 XX Homo sapiens.  
 XX MO2003047611-A2.  
 XX 12-JUN-2003.  
 XX 04-DEC-2002; 2002WC-EP03744.  
 XX 04-DEC-2001; 2001EP-00128844.  
 XX 07-DEC-2001; 2001EP-00129138.  
 XX 07-JUN-2002; 2002EP-00000010.  
 XX (DEVE-) DEVELOPENTWICKLUNGSBIOLOGISCHE FORSCH.  
 XX Meise M, Eulenbergh K, Fritsch R, Haeder T, Broemer G;  
 F1 Steuernagel A;  
 F1 WPI; 2003-532801/50.  
 XX N-PSDB; ACC79776.  
 XX New compositions comprising tyrosine phosphatase PTP10D, protein tyrosine  
 PT kinase Tec or egg-derived tyrosine phosphatase genes or proteins, useful  
 PT for treating or preventing metabolic diseases, e.g. as obesity or  
 PT cachexia.  
 XX Claim 2; Fig. 8B; 83pp; English.  
 XX The present invention describes a pharmaceutical composition comprising a  
 CC nucleic acid (I) protein tyrosine phosphatase PTP10D, non-receptor  
 CC protein tyrosine kinase Tec, egg derived tyrosine phosphatase (EDTP) gene  
 CC family or encoded polypeptide, fragment or variant of nucleic acid  
 CC molecule or polypeptide, an antibody, an aptamer or receptor recognising  
 CC a nucleic acid molecule of PTP10D, Tec, or EDTP gene family or encoded  
 CC polypeptide, and a carrier, diluent and/or adjuvant. The pharmaceutical  
 CC composition can have antidiabetic, hypotensive, cardiant, antihypertensive,  
 CC osteoporotic, cytostatic, anorectic, and immunomodulator activities, and  
 CC can be used in gene therapy. The composition is useful for the  
 CC manufacture of an agent for detecting and/or verifying, for treating and  
 CC alleviating and/or preventing a disorder, including metabolic diseases  
 CC such as obesity and other body weight regulation disorders, as well as  
 CC related disorders such as eating disorder, cachexia, diabetes mellitus,  
 CC hypertension, coronary heart disease, hypercholesterolaemia,  
 CC dyslipidaemia, osteoarthritis, gallstones, cancers (cancers of the  
 CC reproductive organ), sleep apnea, and other diseases, in cells, cell  
 CC masses, organs and/or subjects. The components of the composition may  
 CC also be used in controlling the function of a gene and/or gene product  
 CC which is influenced and/or modified by a PTP10D, Tec, or EDTP homologous  
 CC polypeptide, and for identifying substances capable of interacting with a  
 CC PTP10D, Tec, or EDTP homologous polypeptide. The nucleic acid molecule of  
 CC PTP10D, Tec, or EDTP family or their fragments, may be used in the  
 CC preparation of a non-human animal which over- or under-expresses the  
 CC PTP10D, Tec, or EDTP gene product. The protein sequence represents human  
 CC protein tyrosine phosphatase receptor type B precursor (PTPRB), which is  
 CC a human PTP10B homologous sequence. Human PTPRB is located to chromosome  
 CC 12  
 CC  
 XX Sequence 1997 AA:  
 SQ  
 Query Match 97.0%; Score 1691; DB 7; Length 1997;  
 Best Local Similarity 99.4%; Pred. No. 3,66-179;  
 Matches 312; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 DRPLSVHLNKGKGRKTSCTPIKINQFEGHFKLQADSNVLSKEYELKQVGRNSCDI 61  
 DB 1662 DRPLSVHLNKGKGRKTSCTPIKINQFEGHFKLQADSNVLSKEYELKQVGRNSCDI 1721  
 QY 62 ALPEBNGKRRYNNILPYDARVLSNVDDPCSDYINASYIPGNFRREVITYQGPLPG 121

DB 1722 ALPEBNGKRRYNNILPYDARVLSNVDDPCSDYINASYIPGNFRREVITYQGPLPG 1781  
 QY 122 TRDDPWKWKWKEQVNHVITWQCEKGRKCHWPPADQSLYGGDLLIQGLSSVLPFM 181  
 DB 1782 TRDDPWKWKWKEQVNHVITWQCEKGRKCHWPPADQSLYGGDLLIQGLSSVLPFM 1841  
 QY 182 TRREFKCGESQIDARLIRHFHTWPHGVPETTSLOPRTMRYNRSFGAPV 241  
 DB 1842 TRREFKCGESQIDARLIRHFHTWPHGVPETTSLOPRTMRYNRSFGAPV 1901  
 QY 242 VHCASGVRGTGTIALDRILQQLDSQSVDIYGAHDLRLHRYWVQTECYTHACR 301  
 DB 1902 VHCASGVRGTGTIALDRILQQLDSQSVDIYGAHDLRLHRYWVQTECYTHACR 1961  
 QY 302 DVLARKLRSEQHN 315  
 DB 1962 DVLARKLRSEQHN 1975  
 RESULT 7  
 ADJ70329  
 ID ADJ70329 standard; protein; 1997 AA.  
 XX ADJ70329;  
 XX 06-MAY-2004 (first entry)  
 DE Human heart mitochondrial protein as a therapeutic target SeqID2135.  
 XX  
 XX Human heart mitochondrial protein; diabetes mellitus;  
 KW Huntington's disease; osteoarthritis;  
 KW Leber's hereditary optic neuropathy; LHON;  
 KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;  
 KW myoclonal epilepsy ragged red fibre syndrome; MERRF; cancer;  
 KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;  
 KW osteoporotic; ophthalmological; cytostatic.  
 XX  
 OS Homo sapiens.  
 PN WO2003087768-A2.  
 XX 23-OCT-2003.  
 XX 04-APR-2003; 2003WC-US010870.  
 XX 12-APR-2002; 2002US-0372843P.  
 XX 17-JUN-2002; 2002US-0386987P.  
 XX 20-SEP-2002; 2002US-0412418P.  
 PA (MITO-) MITOKOR.  
 PA (BUCK-) BUCK INST AGE RES.  
 XX Gosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GW;  
 PI Warnock DE;  
 XX WPI; 2003-845369/78.  
 DR  
 XX Identifying a mitochondrial target for drug screening assays and for  
 PT treating diseases associated with altered mitochondrial function;  
 PT comprises detecting a modified polypeptide in a sample and correlating  
 PT with the disease.  
 XX  
 PS Claim 1; SEQ ID NO 2135; 180pp; English.  
 XX This invention relates to novel mitochondrial targets that can be used  
 CC for therapeutic intervention in treating a disease associated with  
 CC altered mitochondrial function. Specifically, it refers to a method for  
 CC identifying proteins of the human heart mitochondrial proteome that are  
 CC useful for drug screening assays, as well as therapeutic targets. The  
 CC present invention describes a method for identifying such proteins that  
 CC can be used in the treatment of various diseases associated with altered  
 CC mitochondrial function including diabetes mellitus, Huntington's disease,

PF 05-FEB-2001; 2001MO-US004098.  
 XX  
 PR 03-FEB-2000; 2000US-00496914.  
 PR 27-APR-2000; 2000US-00560875.  
 PR 20-JUN-2000; 2000US-00598075.  
 PR 19-JUL-2000; 2000US-00620325.  
 PR 01-SEP-2000; 2000US-00654936.  
 PR 15-SEP-2000; 2000US-00663561.  
 PR 20-OCT-2000; 2000US-00693325.  
 PR 30-NOV-2000; 2000US-00728422.  
 XX  
 PA (HUSE-) HYSEQ INC.  
 XX  
 PI Tang YT, Liu C, Dimaac RT, Asundi V, Zhou P, Xu C, Cao Y.  
 PI Ma Y, Zhao Qa, Wang D, Wang J, Ren F, Chen R, Wang ZW,  
 PI Xue J, Yang Y, Wejman T, Goodrich R;  
 PI WPI; 2001-476283/51.  
 DR N-PSDB; AAK52938.  
 XX  
 PT Nucleic acids encoding polypeptides with cytokine-like activities, useful  
 in diagnosis and gene therapy.  
 XX  
 PS Claim 20; Page 340-341; 6221pp; English.  
 CC The invention relates to polynucleotides (AAK51456-AAK53435) and the  
 CC encoded polypeptides (AAK78323-AAK80302) that exhibit activity elating to  
 CC cytokine, cell proliferation or cell differentiation or which may induce  
 CC production of other cytokines in other cell populations. The  
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
 CC peptide therapy. The polypeptides have various cytokine-like activities,  
 CC e.g. stem cell growth factor activity, haematopoiesis regulating  
 CC activity, tissue growth factor activity, immunomodulatory activity and  
 CC activity/inhibin activity and may be useful in the diagnosis and/or  
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
 CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111  
 CC (AAK52582) and 3666 (AAK80020) are omitted as the relevant pages from the  
 CC sequence listing were missing at the time of publication  
 XX  
 SQ Sequence 2002 AA:  
 Query Match 97.0%; Score 1691; DB 4; Length 2002;  
 Best Local Similarity 99.4%; Pred. No. 5, 6e-179;  
 Matches 312; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 DRPLSVHNLGQGNKRTSCPIKINQEGHFMQLQDSNYLLSKEYEELKDVGRNOSCDI 61  
 DB 1667 DRPLSVHNLGQGNKRTSCPIKINQEGHFMQLQDSNYLLSKEYEELKDVGRNOSCDI 1726  
 QY 62 ALLENKGRKNNYLLPYDATRVKLSNVDDPCSDYINASTYIPGNFRREYVVTGPIPG 121  
 DB 1727 ALLENKGRKNNYLLPYDATRVKLSNVDDPCSDYINASTYIPGNFRREYVVTGPIPG 1786  
 QY 122 TDDFMKVMWQVNHNIWVVTQCEKGRVACDHYWPAQDLSLYGDLILQMLSESVLPBW 181  
 DB 1787 TDDFMKVMWQVNHNIWVVTQCEKGRVACDHYWPAQDLSLYGDLILQMLSESVLPBW 1846  
 QY 182 TIREFKTCGEBOLDAHRLIRHFHYTVPDHYGETTOSLIQFVTVRDYINRSPGAPTV 241  
 DB 1847 TIREFKTCGEBOLDAHRLIRHFHYTVPDHYGETTOSLIQFVTVRDYINRSPGAPTV 1906  
 QY 242 VHCASGVGRGTFTALDRITLQOLDSKDSVYIGAVHDLFLRHYVMQTECCQVYLHCVR 301  
 DB 1907 VHCASGVGRGTFTALDRITLQOLDSKDSVYIGAVHDLFLRHYVMQTECCQVYLHCVR 1966  
 QY 302 DVLBARKESEOH 315  
 DB 1967 DVLBARKESEOH 1980

RESULT 10  
 ADO04584  
 ID ADO04584 standard; protein; 312 AA.

XX ADO04584;  
 AC  
 XX 15-JUL-2004 (first entry)  
 DT  
 XX Human HPTbeta truncated intracellular domain (ICD) protein.  
 XX  
 DE Protein co-ordinate data; HPTbeta; HPTP-beta; PTPbeta; PTPbeta; PTPB;  
 XX R-PTP-beta; angiogenesis mediated disorder; diabetic retinopathy;  
 XX sickle cell anemia; Paget's disease; mycobacterial infection;  
 XX systemic lupus erythematosus; myopia; Crohn's disease; psoriasis;  
 XX rheumatoid arthritis; tumour; acquired immune deficiency syndrome; AIDS;  
 XX drug designing; therapy; human; intracellular domain; ICD; mutant;  
 XX mutcin.  
 XX  
 XX Homo sapiens.  
 XX Synthetic.  
 OS  
 XX US2004077065-A1.  
 XX  
 XX 22-APR-2004.  
 XX  
 XX 04-AUG-2003; 2003US-00634027.  
 XX  
 XX 25-SEP-2002; 2002US-0413547P.  
 XX  
 XX (PROC) PROCTER & GAMBLE CO.  
 XX  
 XX Bvdokimov AG, Pokros ME;  
 XX  
 XX WPI; 2004-374235/35.  
 XX N-PSDB; ADO04583.  
 DR  
 XX Identification of compound useful for treatment of angiogenesis mediated  
 FT disorder, by using three-dimensional structure of HPTbeta catalytic  
 FT domain, and employing structure to design, or select compound that binds  
 PT HPTbeta in silico.  
 PT  
 XX  
 XX Disclosure; SEQ ID NO 6; 335pp; English.  
 PS  
 XX The invention relates to the three dimensional coordinates of HPTbeta  
 XX (also known as HPTP-beta, PTPB, PTPbeta, PTPB or R-PTP-beta) protein. It  
 CC also relates to a method for the identification of a compound useful for  
 CC the treatment of an angiogenesis mediated disorder. The compounds  
 CC identified by this method are useful to treat diseases like diabetic  
 CC retinopathy, sickle cell anaemia, Paget's disease, mycobacterial  
 CC infections, systemic lupus erythematosus, myopia, Crohn's disease,  
 CC psoriasis, rheumatoid arthritis, solid or blood borne tumours and  
 CC acquired immune deficiency syndrome (AIDS). The invention is useful for  
 CC the treatment of an angiogenesis mediated disorder or disease. It is also  
 CC useful in drug design techniques. The present sequence is human HPTbeta  
 CC intracellular domain (ICD) truncated protein.  
 CC  
 XX  
 SQ Sequence 312 AA:  
 Query Match 96.9%; Score 1690; DB 8; Length 312;  
 Best Local Similarity 100.0%; Pred. No. 3, 9e-180;  
 Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 DRPLSVHNLGQGNKRTSCPIKINQEGHFMQLQDSNYLLSKEYEELKDVGRNOSCDI 61  
 DB 1 DRPLSVHNLGQGNKRTSCPIKINQEGHFMQLQDSNYLLSKEYEELKDVGRNOSCDI 60  
 QY 62 ALLENKGRKNNYLLPYDATRVKLSNVDDPCSDYINASTYIPGNFRREYVVTGPIPG 121  
 DB 61 ALLENKGRKNNYLLPYDATRVKLSNVDDPCSDYINASTYIPGNFRREYVVTGPIPG 120  
 QY 122 TDDFMKVMWQVNHNIWVVTQCEKGRVACDHYWPAQDLSLYGDLILQMLSESVLPBW 181  
 DB 121 TDDFMKVMWQVNHNIWVVTQCEKGRVACDHYWPAQDLSLYGDLILQMLSESVLPBW 180  
 QY 182 TIREFKTCGEBOLDAHRLIRHFHYTVPDHYGETTOSLIQFVTVRDYINRSPGAPTV 241



PT Use of the polypeptide comprising vascular endothelial-protein tyrosine  
 PT phosphatase (VE-PTP) or the nucleic acid encoding the polypeptide for the  
 PT manufacture of an agent for monitoring or modulating VE-cadherin mediated  
 PT disorders.  
 XX  
 XX Example: Fig 2, Opp, English.  
 XX  
 CC The present invention relates to a polypeptide comprising vascular  
 CC endothelial-protein tyrosine phosphatase (VE-PTP) or its active fragment  
 CC or effector, or the nucleic acid encoding the polypeptide or its  
 CC effector, for use in the manufacture of an agent for monitoring or  
 CC modulating VE-cadherin mediated processes or disorders. The polypeptide  
 CC comprising vascular endothelial-protein tyrosine phosphatase (VE-PTP) or  
 CC its active fragment or effector, or the nucleic acid encoding the  
 CC polypeptide or its effector, is useful for the manufacture of an agent  
 CC for monitoring or modulating VE-cadherin mediated processes or disorders,  
 CC e.g., cancer. The present sequence is a protein shown in the  
 CC exemplification of the invention  
 XX  
 SQ Sequence 1998 AA;  
 Query Match 94.6%; Score 1650; DB 7; Length 1998;  
 Best Local Similarity 95.9%; Pred. No. 2.2e-174;  
 Matches 301; Conservative 8; Mismatches 5; Indels 0; Gaps 0;  
 QY 2 DRPLSVHLNIGQKGRKRTSCPIKINQFEGHFMKLDNSNYLSKEYEELADVGRNOSCDI 61  
 DB 1663 DRPLSVHLNIGQKGRKRTSCPIKINQFEGHFMKLDNSNYLSKEYEELADVGRNOSCDI 1722  
 QY 62 ALPENNKGKRRYNNILPYDASRVKLSNVDDPCSDYINASYIPGNFRREYIVTQGPPLG 121  
 DB 1723 ALPENNKGKRRYNNILPYDASRVKLSNVDDPCSDYINASYIPGNFRREYIVTQGPPLG 1782  
 QY 122 TKDFFWMAWEDONVNIWVTVOCVEKGRVKCDHYWADDPPLYGDLILQWVSESYLPEW 181  
 DB 1783 TKDFFWMAWEDONVNIWVTVOCVEKGRVKCDHYWADDPPLYGDLILQWVSESYLPEW 1842  
 QY 182 TIREFKICSEBOLDHRLIRHFYTWDPHGVPTTOSLIQFRTVDYINRSPGAGPTV 241  
 DB 1843 TIREFKICSEBOLDHRLIRHFYTWDPHGVPTTOSLIQFRTVDYINRSPGAGPTV 1902  
 QY 242 VHCASAGVGTGFIALDRILIQOLDSKDSVDIYGAVHDLRLHVMVWQTECOVYVYLHQCVR 301  
 DB 1903 VHCASAGVGTGFIALDRILIQOLDSKDSVDIYGAVHDLRLHVMVWQTECOVYVYLHQCVR 1962  
 QY 302 DVLARKLRSEOH 315  
 DB 1963 DVLARKLRSEOH 1976  
 Db  
 RESULT 13  
 AAB19773  
 ID AAB19773 standard; protein; 579 AA.  
 XX  
 AC AAB19773;  
 XX  
 DT 19-FEB-2001 (first entry)  
 XX  
 DE Mouse vascular-endothelial protein tyrosine phosphatase.  
 XX  
 KM Vascular-endothelial protein tyrosine phosphatase; VE-PTP; mouse; Tie-2;  
 KM receptor-type tyrosine kinase; antiangiogenic; antitumor;  
 KM antimetastatic; tumour; metastasis; angiogenesis; therapy.  
 XX  
 OS Mus musculus.  
 XX  
 FH Key Location/Qualifiers  
 FT Domain 3..24 "membrane proximal fibronectin II domain"  
 FT Domain 204..223 "note="transmembrane domain"  
 FT Domain 304..549 "note="catalytic domain"

XX  
 XX EPI046715-A1.  
 XX  
 PD 25-OCT-2000.  
 XX  
 PF 23-APR-1999; 99EP-00108074.  
 XX  
 PR 23-APR-1999; 99EP-00108074.  
 XX  
 PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.  
 XX  
 PI Fachinger G, Rissau B, Deutsch U;  
 XX  
 DR WPI; 2000-648932/63.  
 XX  
 DR N-PSDB; AAA88865.  
 XX  
 PT Monitoring or modulating Tie-2 tyrosine kinase activity, useful e.g. for  
 PT regulating tumor growth, using vascular-endothelial protein tyrosine  
 PT phosphatase.  
 XX  
 PS Disclosure; Page 10-12; 60pp; English.  
 XX  
 CC The present sequence is that of murine vascular-endothelial protein  
 CC tyrosine phosphatase (VE-PTP). VE-PTP is a member of subclase III  
 CC receptor type PTPs, bearing fibronectin type III-like repeats in the  
 CC extracellular domain and a single catalytic domain in the cytoplasmic  
 CC tail. VE-PTP specifically interacts with receptor-type tyrosine kinase  
 CC Tie-2, modulating its tyrosine phosphorylation. Tie-2 is involved in  
 CC angiogenic processes, the formation of blood vessels during embryonal  
 CC development, wound healing and in pathological processes such as tumour  
 CC development. VE-PTP or its catalytic domain, nucleic acids and ligands  
 CC can be used to monitor, stimulate or repress Tie-2 activity for the  
 CC purpose of monitoring or modulating angiogenesis, inducing or inhibiting  
 CC vascular growth or remodelling and blood vessel maturation, and  
 CC inhibiting tumour growth and metastasis  
 XX  
 SQ Sequence 579 AA;  
 Query Match 94.3%; Score 1644; DB 3; Length 579;  
 Best Local Similarity 95.5%; Pred. No. 1.5e-174;  
 Matches 300; Conservative 8; Mismatches 6; Indels 0; Gaps 0;  
 QY 2 DRPLSVHLNIGQKGRKRTSCPIKINQFEGHFMKLDNSNYLSKEYEELADVGRNOSCDI 61  
 DB 244 DRPLSVHLNIGQKGRKRTSCPIKINQFEGHFMKLDNSNYLSKEYEELADVGRNOSCDI 303  
 QY 62 ALPENNKGKRRYNNILPYDASRVKLSNVDDPCSDYINASYIPGNFRREYIVTQGPPLG 121  
 DB 304 ALPENNKGKRRYNNILPYDASRVKLSNVDDPCSDYINASYIPGNFRREYIVTQGPPLG 363  
 QY 122 TKDFFWMAWEDONVNIWVTVOCVEKGRVKCDHYWADDPPLYGDLILQWVSESYLPEW 181  
 DB 364 TKDFFWMAWEDONVNIWVTVOCVEKGRVKCDHYWADDPPLYGDLILQWVSESYLPEW 423  
 QY 182 TIREFKICSEBOLDHRLIRHFYTWDPHGVPTTOSLIQFRTVDYINRSPGAGPTV 241  
 DB 424 TIREFKICSEBOLDHRLIRHFYTWDPHGVPTTOSLIQFRTVDYINRSPGAGPTV 483  
 QY 242 VHCASAGVGTGFIALDRILIQOLDSKDSVDIYGAVHDLRLHVMVWQTECOVYVYLHQCVR 301  
 DB 484 VHCASAGVGTGFIALDRILIQOLDSKDSVDIYGAVHDLRLHVMVWQTECOVYVYLHQCVR 543  
 QY 302 DVLARKLRSEOH 315  
 DB 544 DVLARKLRSEOH 557  
 Db  
 RESULT 14  
 AAG78275  
 ID AAG78275 standard; protein; 310 AA.  
 XX  
 AC AAG78275;  
 XX

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 17, 2006, 01:21:14, Search time 41 Seconds

(without alignments)  
748.613 Million cell updates/sec

Title: US-10-634-027-7

Perfect score: 1744

Sequence: 1 GRRPLSVHLNIGOKNRKTS.....VRDVLARKLNSEDRHHHHH 319

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 28346 segs, 9621673 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR 80:\*

1: p1r1:\*

2: p1r2:\*

3: p1r3:\*

4: p1r4:\*

Result No. Score Match Length DB ID Description

Result No.	Score	Match	Length	DB	ID	Description
1	1691	97.0	1997	1	S12050	protein-tyrosine-p
2	1615	92.6	583	2	S17671	protein-tyrosine-p
3	876.5	50.4	1337	1	T36670	protein-tyrosine-p
4	866.5	49.8	1336	2	S68700	HRP beta-like tyr
5	847.5	48.6	1357	2	D41214	protein-tyrosine-p
6	847.5	48.6	1330	2	C41214	protein-tyrosine-p
7	818.5	46.9	1615	2	B49502	protein-tyrosine-p
8	818.5	46.9	1767	2	A49502	protein-tyrosine-p
9	775	44.4	1216	2	S60613	protein-tyrosine-p
10	768	44.0	405	2	I49372	protein-tyrosine-p
11	764	43.8	405	2	S68250	protein-tyrosine-p
12	764	43.8	1226	2	JC7503	protein-tyrosine-p
13	761.5	43.7	1188	1	A57064	protein-tyrosine-p
14	761.5	43.6	1187	1	A57064	protein-tyrosine-p
15	709.5	40.7	1118	1	A53661	protein-tyrosine-p
16	701	40.2	1367	2	T21913	hypothetical prote
17	697.5	40.0	1111	1	A55148	protein-tyrosine-p
18	675	38.7	2302	2	T14328	protein-tyrosine-p
19	618.5	35.5	2314	1	A46151	protein-tyrosine-p
20	615.5	35.3	1445	1	A48148	protein-tyrosine-p
21	610	35.0	1452	1	S17669	protein-tyrosine-p
22	609	34.9	1885	2	T19121	probable protein-t
23	604.5	34.7	1442	1	B48148	protein-tyrosine-p
24	604.5	34.7	1442	1	S17670	protein-tyrosine-p
25	600.5	34.4	1422	2	T42636	protein-tyrosine-p
26	592.5	34.0	1462	1	B48758	protein-tyrosine-p
27	592.5	34.0	1462	1	A48758	protein-tyrosine-p
28	592.5	34.0	1501	2	S18148	protein-tyrosine-p
29	592.5	34.0	1663	2	S46217	protein-tyrosine-p

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

30	592	33.9	1290	2	A56493	leucocyte common a
31	591.5	33.9	1907	2	S50893	protein-tyrosine-p
32	590	33.8	1457	1	A48066	protein-tyrosine-p
33	589	33.8	796	1	JC1285	protein-tyrosine-p
34	589	33.8	802	1	A36065	protein-tyrosine-p
35	589	33.8	1440	2	JC6312	protein-tyrosine-p
36	588	33.7	1898	2	S46216	leukocyte antigen-
37	587.5	33.7	832	2	JC8051	protein tyrosine p
38	586.5	33.6	1301	1	A41622	protein-tyrosine-p
39	586	33.6	1897	1	TDHLLK	leukocyte antigen-
40	583.5	33.5	1912	2	A56178	protein-tyrosine-p
41	582.5	33.5	1437	2	T31093	probable protein-t
42	581	33.4	582	2	A57068	protein-tyrosine-p
43	580.5	33.3	1459	2	I50212	protein-tyrosine-p
44	578.5	33.2	2029	1	TDFEUK	protein-tyrosine-p
45	577.5	33.1	1691	1	D54689	protein-tyrosine-p

## ALIGNMENTS

## RESULT 1

S12050 protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type beta precursor - human

C/Species: Homo sapiens (man)

C/Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text\_change 09-Jul-2004

C/Accession: S12050; S15818; S15819

R/Krueger, N.X.; Streuli, M.; Saito, H.

EMBO J. 9, 3241-3252, 1990

A/Title: Structural diversity and evolution of human receptor-like protein tyrosine phs

A/Reference number: S12049; MUID:91006018; PMID:2170109

A/Accession: S12050

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1997 <KRU>

A/Cross-references: UNIPROT: P23467; UNIPARC: UP10000034765; GB: X54131; NID: g35787; PIDN: RDe Vries, L.; Li, R.Y.; Ragab, A.; Ragab-Thomas, J.M.F.; Chap, H.

FEBS Lett. 282, 281-288, 1991

A/Title: Expression of a truncated protein-tyrosine phosphatase mRNA in human lung.

A/Reference number: S15818; MUID:91243813; PMID:1645282

A/Accession: S15818

A/Status: not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1872-1997 <VR2>

A/Cross-references: UNIPARC: UP10000173861

A/Status: not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1872-1997 <VR2>

A/Cross-references: UNIPARC: UP10000173861

A/Status: not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1872-1997 <VR2>

A/Cross-references: UNIPARC: UP10000173861

A/Status: not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1872-1997 <VR2>

A/Cross-references: UNIPARC: UP10000173861

Query Match 97.0%; Score 1691; DB 1; Length 1997;  
Best Local Similarity 99.4%; Pred. No. 3e-137;  
Matches 312; Conservative 1; Mismatches 1; Gaps 0;

DB 2 DBPLSVHLNIGOKNRKTSCKIKINQFEGHFWKQADSNVLSKEYELKQDVGNOSCDI 61  
1662 DBPLSVHLNIGOKNRKTSCKIKINQFEGHFWKQADSNVLSKEYELKQDVGNOSCDI 1721

Db 1194 PL-RQFHTSMHPGVDPDTDLINFRYLVRDYMKSPPESPIVHCAGVGRGTFTAI 1252

Qy 258 DRIIOQSDSDVDYIGAVHDLRLHRVHWVQECQYVYLHQCVRDVLARK 308

Db 1253 DRLIYQIENNTVYDYGIVYDLRMRHPLVWQEDQYVFLNQCVDLIVASOK 1303

## RESULT 4

SR6700

HTP beta-like tyrosine phosphatase precursor - mouse

C/Species: Mus musculus (house mouse)

C/Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004

C/Accession: S68700

R/Kuramochi, S.; Matsuda, S.; Matsuda, Y.; Saitoh, T.; Ohnogi, M.; Yamamoto, T.

FEBS Lett. 378, 7-14, 1996

A/Title: Molecular cloning and characterization of BTP, a murine receptor-type tyrosine

A/Reference number: S68700; MUID:96140699; PMID:8549806

A/Accession: S68700

A/Status: preliminary; nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-1238 <KUR>

A/Cross-references: UNIPROT:Q64455; UNIPARC:UPI00000013C2; GB:D45212; NID:G1208432; PIDN

C/Genetics:

A/Map position: 281-2

C/Suprafamily: protein-tyrosine-phosphatase, receptor type J; fibronectin type III repeats

C/Keywords: phosphoprotein

F/1-28/Domain: signal sequence #status predicted <SIG>

F/29-138/Product: HTP beta-like tyrosine phosphatase #status predicted <MAT>

F/267-1348/Domain: fibronectin type III repeat homology <3PR>

F/966-1188/Domain: protein-tyrosine-phosphatase homology <PTP>

F/1140/Active site: Cys (phosphocysteine intermediate) #status predicted

F/1146/Binding site: substrate phosphate (Arg) #status predicted

Query Match 49.8%; Score 868.5; DB 2; Length 1238;

Best Local Similarity 55.7%; Pred. No. 1.7e-66;

Matches 162; Conservative 56; Mismatches 70; Indels 3; Gaps 3;

Qy 18 KTSCPIKINQFEGHMKQADSNVILSKYEELKDVGNOSCDIALPENRGNRYNNIL 77

Db 917 KKSILIVENFEHYRFXKQADSNCGFAEYEDLKIGSLPKYLAIEKNNKRNRYNNIL 976

Qy 78 PYDARVKSNDVDDPCSDYINASYI RGNPFREYITQSGIPGKDDPFWMVQGNVYN 137

Db 977 FIDISRYVLS-VQTHSTDPITNANMFGHSGKQPIATQGPILNLIKDPFWMVQGNVYN 1035

Qy 138 IVMVTCCEKGRVCDHYMPADDSLYGDDLIQMSSEVLPENTIREFKICGEQDLAH 197

Db 1036 IVMILTKCEVGGRTKEEYWPESKO-ADQYCDITVAVTSVLPENTIRDFVKNQMSSEH 1094

Qy 198 RLIFHFYTWDPHGVPEPTQSILQFVKTVDYINRSPGAPTVHCSAGVGRGTFTAI 257

Db 1095 PL-RQFHTSMHPGVDPDTDLINFRYLVRDYMKSQIPESPPIVHCAGVGRGTFTAI 1153

Qy 258 DRIIOQSDSDVDYIGAVHDLRLHRVHWVQECQYVYLHQCVRDVLARK 308

Db 1154 DRLIYQIENNTVYDYGIVYDLRMRHPLVWQEDQYVFLNQCVDLIVASOK 1204

## RESULT 5

D41214

Protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type 10D, short splice form precursor

C/Species: Drosophila melanogaster

C/Date: 28-May-1992 #sequence\_revision 28-May-1992 #text\_change 09-Jul-2004

C/Accession: D41214; A41215

C/Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; rec

F/1197-1213/Domain: intracellular #status predicted <INT>

F/1214-1515/Domain: protein-tyrosine-phosphatase homology <PTP>

F/1473/Active site: Cys (phosphocysteine intermediate) #status predicted

F/1473/Binding site: substrate phosphate (Arg) #status predicted

A/Title: Two Drosophila receptor-like tyrosine phosphatase genes are expressed in a sube

A/Reference number: A41214; MUID:92034988; PMID:1657401

A/Accession: D41214

A/Status: nucleic acid sequence not shown; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-1557 <YAN>

A/Cross-references: UNIPROT:P35992; UNIPARC:UPI0000177055; GB:M80465

R/Tian, S.S.; Tsoulfas, P.; Zimm, K.

Cell 67, 675-685, 1991

A/Title: Three receptor-linked protein-tyrosine phosphatases are selectively expressed

A/Reference number: A41215; MUID:92034988; PMID:1657402

A/Accession: A41215

A/Molecule type: mRNA

A/Residues: 1-904; 'L', 906-1125, 'Q', 1126-1165, 'YR', 1168-1171, 'N', 1173-1215, 'L', 1217-141

A/Cross-references: UNIPARC:UPI00000281D9; GB:M80538; NID:G158644; PIDN:AAA28952.1; P

C/Genetics:

A/Genes: FlyBase:FlyBase:FBgn0004370

A/Cross-references: FlyBase:FBgn0004370

C/Suprafamily: protein-tyrosine-phosphatase, receptor type 4B; fibronectin type III r

C/Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; rec

F/1197-1213/Domain: intracellular #status predicted <INT>

F/1214-1515/Domain: protein-tyrosine-phosphatase homology <PTP>

F/1473/Active site: Cys (phosphocysteine intermediate) #status predicted

F/1473/Binding site: substrate phosphate (Arg) #status predicted

Query Match 48.6%; Score 847.5; DB 2; Length 1557;

Best Local Similarity 55.6%; Pred. No. 1.5e-64;

Matches 160; Conservative 45; Mismatches 76; Indels 7; Gaps 3;

Qy 22 PIKIQFEGHMKQADSNVILSKYEELKDVGNOSCDIALPENRGNRYNNILPYDA 81

Db 1250 PILINQFAHYRLMSADSPFRSEFEELKHVGRDQCTPADLPCNRPRNFTVILPYDH 1309

Qy 82 TVYKLSNDDPCSDYINASYI RGNPFREYITQSGIPGKDDPFWMVQGNVYNV 141

Db 1310 SFKIQPDDDESIDYINANVPRHNSPREFLVIGSLHSTRDDPFWMVQGNVYNV 1369

Qy 142 TVCEKGRVCDHYMPADDSLYGDDLIQMSSEVLPENTIREFKICGEQDLAHRI 200

Db 1370 TVCEKGRVCDHYMPADDSLYGDDLIQMSSEVLPENTIREFKICGEQDLAHRI 1425

Qy 201 RHFHYTWDPHGVPEPTQSILQFVKTVDYINRSPGAPTVHCSAGVGRGTFTAI 260

Db 1426 RHFHYTWDPHGVPEPTQSILQFVKTVDYINRSPGAPTVHCSAGVGRGTFTAI 1483

Qy 261 LQQLSDSDVDYIGAVHDLRLHRVHWVQECQYVYLHQCVRDVLARK 308

Db 1484 LQQLSDSDVDYIGAVHDLRLHRVHWVQECQYVYLHQCVRDVLARK 1531

## RESULT 6

C41214

Protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type 10D, long splice form precursor

C/Species: Drosophila melanogaster

C/Date: 28-May-1992 #sequence\_revision 12-Jun-1992 #text\_change 24-Apr-1998

C/Accession: C41214

C/Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; rec

F/1197-1213/Domain: intracellular #status predicted <INT>

F/1214-1515/Domain: protein-tyrosine-phosphatase homology <PTP>

F/1473/Active site: Cys (phosphocysteine intermediate) #status predicted

F/1473/Binding site: substrate phosphate (Arg) #status predicted

A/Title: Two Drosophila receptor-like tyrosine phosphatase genes are expressed in a s

A/Reference number: A41214; MUID:92034988; PMID:1657401

A/Accession: C41214

A/Status: nucleic acid sequence not shown; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-1630 <YAN>

A/Cross-references: UNIPARC:UPI0000177054; GB:M80465

C/Genetics:

A/Genes: FlyBase:FlyBase:FBgn0004370

A/Cross-references: FlyBase:FBgn0004370

C/Suprafamily: protein-tyrosine-phosphatase, receptor type 4B; fibronectin type III r

C/Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; rec

F/1197-1213/Domain: intracellular #status predicted <INT>

F/1214-1515/Domain: protein-tyrosine-phosphatase homology <PTP>

F/1473/Active site: Cys (phosphocysteine intermediate) #status predicted

F/1473/Binding site: substrate phosphate (Arg) #status predicted

Query Match 48.6%; Score 847.5; DB 2; Length 1600;

Best Local Similarity 55.6%; Pred. No. 1.6e-64;

Matches 160; Conservative 45; Mismatches 76; Indels 7; Gaps 3;

F/30-818/Domain: extracellular #status predicted <EXT>  
 F/30-118/Domain: fibronectin type III repeat homology #status atypical <FN3A>  
 F/116-209/Domain: fibronectin type III repeat homology #status atypical <FN3B>  
 F/328-445/Domain: fibronectin type III repeat homology <FN3>  
 F/431-519/Domain: fibronectin type III repeat homology <FN3B>  
 F/528-625/Domain: fibronectin type III repeat homology <FN3B>  
 F/630-713/Domain: fibronectin type III repeat homology <FN3G>  
 F/721-810/Domain: fibronectin type III repeat homology <FN3G>  
 F/811-1187/Domain: fibronectin type III repeat homology <FN3G>  
 F/811-875, 876-1187/Domain: fibronectin type III repeat homology <FN3G>  
 F/813-843/Domain: fibronectin type III repeat homology <FN3G>  
 F/843-1187/Domain: fibronectin type III repeat homology <FN3G>  
 F/901-1187/Domain: fibronectin type III repeat homology <FN3G>  
 F/933-1155/Domain: fibronectin type III repeat homology <FN3G>  
 F/735,154,189,201,227,277,286,323,369,460,489,699,711,732,789/Binding site: carbohydrate  
 F/1107/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F/1113/Binding site: substrate phosphate (Arg) #status predicted

Query Match 43.6%; Score 760.5; DB 1; Length 1187;  
 Best Local Similarity 49.8%; Pred. No. 3.3e-57;  
 Matches 143; Conservative 56; Mismatches 81; Indels 7; Gaps 3;

QY 17 RTSCPIKINQFGHFMKLDQSNVLSKYEELKQVGRNOSCDIALPENRGKRNIN 76  
 DB 883 RLTLNTPVQLDDPAYIKOMAKDSYKSLQFELKLGIDIPFADJPLNRCGRYVNI 942  
 QY 77 LRYDAITKSNVDDPCSDYINASTYFGNNFRREYITQGLPGTKDPKQVMEQVNI 136  
 DB 943 LYPDSEKRLSKNEBEGADYINASTYFGNNFRREYITQGLPGTKDPKQVMEQVNI 1002  
 QY 137 NIVMTQVCEKGVKCDHWPRADDSLYGVDLILQMLSESVLEWITREPKICEBOLA 196  
 DB 1003 KIVMTQVCEKGVKCDHWPRADDSLYGVDLILQMLSESVLEWITREPKICEBOLA 1059  
 QY 197 HRLNRPHTVDPHGV-ETTSLLIQFRTVYDYNRSFGAGPTVVCAGVGTGTF 254  
 DB 1060 WQDVNHRVYDYNRSFGAGPTVVCAGVGTGTF 1117  
 QY 255 IALDRILQQLDSKSDYIGAVHDLRLHVMVQTECOVYLIHQCV 301  
 DB 1118 IALDRILQQLDSKSDYIGAVHDLRLHVMVQTECOVYLIHQCV 1164

## RESULT 15

A49724  
 protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type H precursor - human  
 N.Alternate names: protein-tyrosine-phosphatase, stomach cancer-associated type 1, SAP-1  
 C.Species: Homo sapiens (man)  
 C.Date: 03-May-1994 #sequence\_revision 23-Feb-1996 #text\_change 09-Jul-2004  
 C.Accession: A49724  
 R.Matuzaki, T.; Suzuki, T.; Uchida, T.; Inazawa, J.; Ariyama, T.; Matsuda, K.; Horita, K.  
 J. Biol. Chem. 269, 2075-2081, 1994  
 A.Title: Molecular cloning of a human transmembrane-type protein tyrosine phosphatase ar  
 A.Reference number: A49724; MIM:145451; PMID:8294453  
 A.Accession: A49724  
 A.Molecule type: mRNA  
 A.Residues: 1-1118 <M10>  
 A.Cross-references: UNIPROT: Q15426; UNIPARC: UPI0000073BF2; GB: D15049; NID: 9475003; PTDN:  
 C.Genetics:  
 A.Gene: GDB:PTPH; SAP-1  
 A.Cross-references: GDB:305504  
 A.Map position: 19q13.4-19q13.4  
 A.Note: highly expressed in colon and pancreatic cancer cells but not in the normal cell  
 C.Superfamily: protein-tyrosine-phosphatase, receptor type H; fibronectin type III repeat  
 C.Keywords: carcinogenesis; duplication; glycoprotein; phosphoprotein; phosphoric moieties  
 F.1-27/Domain: signal sequence #status predicted <SIG>  
 F.27-110/Domain: fibronectin type III repeat homology <3FNA>  
 F.28-118/Domain: fibronectin type III repeat homology <EXT>  
 F.28-118/Domain: fibronectin type III repeat homology <EXT>  
 F.116-199/Domain: fibronectin type III repeat homology <3FNB>  
 F.205-289/Domain: fibronectin type III repeat homology <3FNC>  
 F.296-379/Domain: fibronectin type III repeat homology <3FND>  
 F.385-468/Domain: fibronectin type III repeat homology <3FNE>

F/474-558/Domain: fibronectin type III repeat homology <3FNE>  
 F/564-658/Domain: fibronectin type III repeat homology <3FNG>  
 F/667-737/Domain: fibronectin type III repeat homology <3FNE>  
 F/762-778/Domain: fibronectin type III repeat homology <3FNE>  
 F/779-1118/Domain: fibronectin type III repeat homology <3FNE>  
 F/846-1070/Domain: fibronectin type III repeat homology <3FNE>  
 F/935,78,83,107,132,149,172,196,203,286,304,312,329,352,376,383,401,436,439,470,490,558  
 F/1028/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F/1028/Binding site: substrate phosphate (Arg) #status predicted

Query Match 40.7%; Score 709.5; DB 1; Length 1118;  
 Best Local Similarity 48.0%; Pred. No. 7.8e-53;  
 Matches 134; Conservative 47; Mismatches 95; Indels 3; Gaps 2;

QY 23 IKINQEGHFMKLDQSNVLSKYEELKQVGRNOSCDIALPENRGKRNINLPYAT 82  
 DB 802 IPADPADVHAKERDSNGFADYQSLVGSQSNVASTANAKRNINLPYAT 861  
 QY 83 RYKLSNVDDPCSDYINASTYFGNNFRREYITQGLPGTKDPKQVMEQVNI 142  
 DB 862 RYKLSNVDDPCSDYINASTYFGNNFRREYITQGLPGTKDPKQVMEQVNI 921  
 QY 143 QVCEKGVKCDHWPRADDSLYGVDLILQMLSESVLEWITREPKICEBOLA 201  
 DB 922 NCEAGRYVCEHWPRADDSLYGVDLILQMLSESVLEWITREPKICEBOLA 979  
 QY 202 HRYTVDPHGVPTTQSLIQFRTVYDYNRSFGAGPTVVCAGVGTGTFIALDRIL 261  
 DB 980 QFYQAMPDHGVPTTQSLIQFRTVYDYNRSFGAGPTVVCAGVGTGTFIALDRIL 1039  
 QY 262 QQLDSKSDYIGAVHDLRLHVMVQTECOVYLIHQCV 300  
 DB 1040 QQLDSKSDYIGAVHDLRLHVMVQTECOVYLIHQCV 1078

Search completed: February 17, 2006, 01:25:38  
 Job time: 43 secs

RG Genoscope, Whitehead Institute Centre for Genome Research;  
 RL Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.  
 CC -!- CAUTION: The sequence shown here is derived from an  
 EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is  
 preliminary data.  
 CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is  
 preliminary data.  
 DR EMBL, CA001007048; CAP9510.1; -; Genomic DNA.  
 DR InterPro: IPR003961; FN\_111.  
 DR InterPro: IPR003595; PTPC\_motif.  
 DR InterPro: IPR00387; TYR\_phosphatase.  
 DR InterPro: IPR00242; Tyr\_PP.  
 DR Pfam: PF00041; fn3; 14.  
 DR Pfam: PF00102; Y\_phosphatase; 1.  
 DR PRINTS: PR00700; PRTYPHPTASE.  
 DR SMART: SM00060; FN3; 14.  
 DR SMART: SM00194; PTPC; 1.  
 DR SMART: SM00404; PTPC\_motif; 1.  
 DR PROSITE: PS00853; FN3; 14.  
 DR PROSITE: PS00383; TYR\_PHOSPHATASE\_1; 1.  
 DR PROSITE: PS00056; TYR\_PHOSPHATASE\_2; 1.  
 DR PROSITE: PS00055; TYR\_PHOSPHATASE\_PTP; 1.  
 KM Hydrolyase.  
 FT NON\_TER 1 1  
 FT SEQUENCE 1991 AA; 214280 MW; ABECSF629DD27A78 CRC64;  
 SQ  
 Query Match 67.6%; Score 1178.5; DB 2; Length 1991;  
 Best Local Similarity 69.8%; Pred. No. 9,4e-90;  
 Matches 213; Conservative 35; Mismatches 46; Indels 9; Gaps 1;  
 QY 9 LNLGKGRKRTSCPIKINGFCHMKLQADSNYLLSKYEYELKDVGNOSCDIALLPENR 68  
 DB 1679 LVYGVRSRRVGSFVYAGQFQHDLDLSSVLLSEFEDLDVGRNADVAVRPENR 1738  
 QY 69 GGRYNNILPYDARTVKLSNVDDPCSDYINASYIPGNRRERYIVTGPPLPTKDDFK 128  
 DB 1739 GGRYNNILPYDARTVKLSNVDDPCSDYINASYIPGNRRERYIVTGPPLPTKDDFK 1798  
 QY 129 WMEQONVNIIVMTQCEKGRVCKDHYMPADODSLYYGDLILQMLSESVLPWTIREFKI 188  
 DB 1799 WMEQONVNIIVMTQCEKGRVCKDHYMPADODSLYYGDLILQMLSESVLPWTIREFKI 1849  
 QY 189 CEEBGLAHRLRHPHYTWMPDHGVPETTSILQFRTVVDYINRSPGAGTVVHCSAGV 248  
 DB 1850 SESEGCAPRLRHPHYTWMPDHGVPETTSILQFRTVVDYINRSPGAGTVVHCSAGV 1909  
 QY 249 GRTGFTALRLTIQDLSDKSDVDIYGAVHDLRLHRYVMQTECOVYVILHOCVRDYLARK 308  
 DB 1910 GRTGFTALRLTIQDLSDKSDVDIYGAVHDLRLHRYVMQTECOVYVILHOCVRDYLARK 1969  
 QY 309 LRSBQ 313  
 DB 1970 HRGBO 1974  
 Db  
 RESULT 7  
 Q9W6V5 CHICK PRELIMINARY; PRT; 1406 AA.  
 ID Q9W6V5;  
 AC Q9W6V5;  
 DT 01-NOV-1999 (TREMBLrel. 12, Created)  
 DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Supporting-cell antigen precursor.  
 OS Gallus gallus (Chicken).  
 OC Birkayocia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus  
 NCBI\_TaxID=9031;  
 RN NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Intestine;  
 RX MEDLINE=99296852; PubMed=10366616;  
 RA Kruger R.P., Goodyear R.J., Legan P.K., Warchol M., Raphael Y.,  
 Cotanche D.A., Richardson G.P.;

RT "The supporting-cell antigen: a receptor-like protein tyrosine  
 RT phosphatase expressed in the sensory epithelia of the inner ear."  
 RL J. Neurosci. 15:4815-4827(1999).  
 RN [2]  
 RP TISSUE=Intestine;  
 RC NUCLEOTIDE SEQUENCE.  
 RA Legan P.K.,  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).  
 DR EMBL, AJ238216; CAB41885.2; -; mRNA.  
 DR HSP, P18052; IYFO.  
 DR EMBL: ENSGALG0000006392; Gallus gallus.  
 DR GO: GO:0016021; C: integral to membrane; IEA.  
 DR GO: GO:0016787; F: hydrolyase activity; IEA.  
 DR GO: GO:0004725; F: protein tyrosine phosphatase activity; IEA.  
 DR GO: GO:0006470; P: protein amino acid dephosphorylation; IEA.  
 DR InterPro: IPR003961; FN\_111.  
 DR InterPro: IPR00387; TYR\_phosphatase.  
 DR InterPro: IPR00242; Tyr\_PP.  
 DR Pfam: PF00041; fn3; 9.  
 DR Pfam: PF00102; Y\_phosphatase; 1.  
 DR PRINTS: PR00700; PRTYPHPTASE.  
 DR SMART: SM00060; FN3; 9.  
 DR PROSITE: PS00853; FN3; 10.  
 DR PROSITE: PS00383; TYR\_PHOSPHATASE\_1; 1.  
 DR PROSITE: PS00056; TYR\_PHOSPHATASE\_2; 1.  
 DR PROSITE: PS00055; TYR\_PHOSPHATASE\_PTP; 1.  
 KM Hydrolyase; Receptor; Signal; Transmembrane.  
 FT SIGNAL 1 24  
 FT SEQUENCE 1406 AA; 154213 MW; 2D609885C0F367B CRC64;  
 SQ  
 Query Match 51.0%; Score 889.5; DB 2; Length 1406;  
 Best Local Similarity 55.3%; Pred. No. 1.3e-65;  
 Matches 162; Conservative 60; Mismatches 64; Indels 7; Gaps 4;  
 QY 18 KTSCKPIKINGFCHMKLQADSNYLLSKYEYELKDVGNOSCDIALLPENRGRYNNIL 77  
 DB 1085 KSKIMKYENESYFKKQADSNCGFAEYELKSAVGHQKFAAIAIRGRKRYNNIL 1144  
 QY 78 PYDATVKLSNVDDPCS--DYINASYIPGNRRERYIVTGPPLPTKDDFKWMEQONV 135  
 DB 1145 PYDISRVKLSN--PCTTDDYINANVMPGYSKAFIAQGPLPTIIDEFWRMIMWKNI 1201  
 QY 136 HNIVMTQCEKGRVCKDHYMPADODSLYYGDLILQMLSESVLPWTIREFKICEBOLD 195  
 DB 1202 YSLVMTLCVGRARTCEGYMP-DKQSKSYGDIIVTVVSEVLPWTIRDFVENVADTME 1260  
 QY 196 AHELRLRHPHYTWMPDHGVPETTSILQFRTVVDYINRSPGAGTVVHCSAGVGRGTGFI 255  
 DB 1261 SH-TVQGHFTSMVDHGVETTDLLINRHLVHYSQNPIDSPILVHCSAGVGRGTGFI 1319  
 QY 256 ALDRILQDLSDKSDVDIYGAVHDLRLHRYVMQTECOVYVILHOCVRDYLARK 308  
 DB 1320 ALDRILQDLSDKSDVDIYGAVHDLRLHRYVMQTECOVYVILHOCVRDYLARK 1372  
 Db  
 RESULT 8  
 PTPRJ HUMAN  
 ID PTPRJ HUMAN  
 AC Q12913; Q12913; Q8NRM2;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Receptor-type tyrosine-protein phosphatase eta precursor (EC 3.1.3.48)  
 DE (Protein-tyrosine phosphatase eta) (R-PTP-eta) (HPTP eta) (Protein-  
 DE tyrosine phosphatase receptor type J) (Densily enhanced phosphatase 1)  
 DE (DEP-1) (CD148 antigen).  
 GN Name=PTPJ; Synonyms=DEP1;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Buthontoglires; Primates; Catarrhini; Hominiidae;  
 OC Homo



FT VARIANT 214 214 R -> C (in colon cancer; somatic  
 mutation)  
 FT 276 276 Q -> F (in colon cancer; somatic  
 mutation; dbSNP:1566734).  
 FT VARIANT 276 276  
 FT CONFLICT 261 261 G -> D (in Ref. 1).  
 FT CONFLICT 918 929 YNGKLESLGSYR -> LOWEAGTSGLLP (in Ref. 2).  
 SQ SEQUENCE 1337 AA; 145927 MW; E6752D52C4B6AFE CRC64;  
 Query Match 50.4%; Score 878.5; DB 1; Length 1337;  
 Best Local Similarity 56.4%; Pred. No. 1e-64;  
 Matches 164; Conservative 56; Mismatches 68; Indels 3; Gaps 3;  
 QY 18 KTSCEPKINGEFGHFKLQADSNYLLSKYEELKDVGNOSCDIALPENRGNKRYNNIL 77  
 DB 1016 KSKSLIRVENFEAFYFKQADSNCGFAEEYEDKLVGISQRYAELANRGNKRYNNVL 1075  
 QY 78 PYDATRYVLSNVDDPCSDYINASYIPGNFRREYIVTQGPLGTQDDPFWKWEQVYN 137  
 DB 1076 PYDISRYVLS-VQTHSTDYINANVMGHSKKDFIATQGPLNTLKQPFWMWEKQVYA 1134  
 QY 138 IVMATCYEGRKVCCHWYAPADOSLYYGDLLIOMLSSEYLPENTIREFKICGEOLDIAH 197  
 DB 1135 IVMATCYEGRKVCCHWYAPADOSLYYGDLLIOMLSSEYLPENTIREFKICGEOLDIAH 1193  
 QY 198 RLIRHRYTWPDPHGPETTSLSIQFVRYVDYINRSPGAGPTVWCHSAGVGTGTFTAL 257  
 DB 1194 PL-RQHFHTSPDHGVPDITDLINFRYLVDMQKQPSPEPFLVWCHSAGVGTGTFTAL 1252  
 QY 258 DRLIQQLDSKDSVDYIGAVHDLRLHRYVMVQTECOYVYLHQCVRDYLARK 308  
 DB 1253 DRLIYQIENNTVDYIGVYDILRMHRLPMVQTEDOYVFLNQCVDLIVRSOK 1303  
 RESULT 9  
 Q6K302 MOUSE PRELIMINARY; PRT; 1238 AA.  
 ID Q6K302.1  
 AC Q6K302.1  
 DT 01-OCT-2002 (Tremblrel. 22, Created)  
 DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)  
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
 DE PPRPT.  
 GN Name=Peprj.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=STS;  
 RA van Wezel T., Ruijvenkamp C.A.B., Zanon C., Stassen A.P.M., Vleck C.,  
 RA Ceikos T., Tripodis N., Groot P.C., Dauwerse H., van Ommen G.J.B.,  
 RA Demant P.;  
 RA Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 RL -1- SUBCELLULAR LOCATION: Type I membrane protein (by similarity).  
 CC EMBL: AY039232; AAK98640.1; -; mRNA.  
 DR HSSP: P18052; IYFO.  
 DR MGI: MGI:104574; Peprj.  
 DR GO: GO:0005615; C:extracellular space; TAS.  
 DR GO: GO:0016021; C:integral to membrane; TAS.  
 DR GO: GO:0007507; P:heart development; IMP.  
 DR GO: GO:0001570; P:vasculogenesis; IMP.  
 DR InterPro: IPR000387; TYR\_PP.  
 DR InterPro: IPR000242; TYR\_PP.  
 DR Pfam: PF00102; Y\_phosphatase; 1.  
 DR Pfam: PF00041; fnj\_6.  
 DR PRINTS: PR00700; PRTYPHPTASE.  
 DR SMART: SM00060; PTPC; 1.  
 DR SMART: SM00194; PTPC; 7.  
 DR SMART: PS00853; FNJ; 7.  
 DR PROSITE: PS00853; FNJ; 7.

DR PROSITE: PS00853; TYR\_PHOSPHATASE\_1; 1.  
 DR PROSITE: PS00856; TYR\_PHOSPHATASE\_2; 1.  
 DR PROSITE: PS00855; TYR\_PHOSPHATASE\_PTP; 1.  
 KY Hydrolyase; Repeat; Transmembrane.  
 SQ SEQUENCE 1238 AA; 136772 MW; 0D02F5HFE8E23C0B2 CRC64;  
 Query Match 49.9%; Score 869.5; DB 2; Length 1238;  
 Best Local Similarity 55.7%; Pred. No. 5.4e-64;  
 Matches 162; Conservative 56; Mismatches 70; Indels 3; Gaps 3;  
 QY 18 KTSCEPKINGEFGHFKLQADSNYLLSKYEELKDVGNOSCDIALPENRGNKRYNNIL 77  
 DB 917 KSKSLIRVENFEAFYFKQADSNCGFAEEYEDKLVGISQRYAELANRGNKRYNNVL 976  
 QY 78 PYDATRYVLSNVDDPCSDYINASYIPGNFRREYIVTQGPLGTQDDPFWKWEQVYN 137  
 DB 977 PYDISRYVLS-VQTHSTDYINANVMGHSKKDFIATQGPLNTLKQPFWMWEKQVYA 1035  
 QY 138 IVMATCYEGRKVCCHWYAPADOSLYYGDLLIOMLSSEYLPENTIREFKICGEOLDIAH 197  
 DB 1036 IVMATCYEGRKVCCHWYAPADOSLYYGDLLIOMLSSEYLPENTIREFKICGEOLDIAH 1094  
 QY 198 RLIRHRYTWPDPHGPETTSLSIQFVRYVDYINRSPGAGPTVWCHSAGVGTGTFTAL 257  
 DB 1095 PL-RQHFHTSPDHGVPDITDLINFRYLVDMQKQPSPEPFLVWCHSAGVGTGTFTAL 1153  
 QY 258 DRLIQQLDSKDSVDYIGAVHDLRLHRYVMVQTECOYVYLHQCVRDYLARK 308  
 DB 1154 DRLIYQIENNTVDYIGVYDILRMHRLPMVQTEDOYVFLNQCVDLIVRSOK 1204  
 RESULT 10  
 Q6L373 MOUSE PRELIMINARY; PRT; 361 AA.  
 ID Q6L373.1  
 AC Q6L373.1  
 DT 01-NOV-1996 (Tremblrel. 01, Created)  
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
 DE Protein tyrosine phosphatase (frAGMENT).  
 GN Name=Peprj; Synonyms=PTP-RL9;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=CS7/B6; Tissue=liver;  
 RA Higashitsuji H., Arai S., Furutani M., Imamura M., Kaneko Y.,  
 RA Takenawa J., Nakayama H., Fujita U.,  
 RT Enhanced expression of multiple protein tyrosine phosphatases in the  
 RT regenerating mouse liver: Isolation of PTP-RL 10, a novel  
 RT cytoplasmic-type phosphatase with sequence homology to cytoskeletal  
 RT protein 4.1.";  
 RT Oncogene 0:0-0(1995).  
 RL EMBL: D49393; BAA08386.1; -; mRNA.  
 DR HSSP: P18052; IYFO.  
 DR MGI: MGI:104574; Peprj.  
 DR GO: GO:0005615; C:extracellular space; TAS.  
 DR GO: GO:0016021; C:integral to membrane; TAS.  
 DR GO: GO:0007507; P:heart development; IMP.  
 DR GO: GO:0001570; P:vasculogenesis; IMP.  
 DR InterPro: IPR000387; TYR\_PP.  
 DR InterPro: IPR000242; TYR\_PP.  
 DR Pfam: PF00102; Y\_phosphatase; 1.  
 DR PRINTS: PR00700; PRTYPHPTASE.  
 DR SMART: SM00194; PTPC; 1.  
 DR PROSITE: PS00853; TYR\_PHOSPHATASE\_1; 1.  
 DR PROSITE: PS00856; TYR\_PHOSPHATASE\_2; 1.  
 DR PROSITE: PS00855; TYR\_PHOSPHATASE\_PTP; 1.  
 KY Hydrolyase.  
 FT NON TER 1 1  
 SQ SEQUENCE 361 AA; 41726 MW; B514628BD1023AA CRC64;

Query Match 49.8%; Score 868.5; DB 2; Length 361;  
 Best Local Similarity 55.7%; Pred. No. 1.3e-64;  
 Matches 162; Conservative 56; Mismatches 70; Indels 3; Gaps 3;

DB 18 KTSCEPIKINGEFGHFKMLQADSNVLSKEYEELKDVGRNOSCDIALPENNGKRRNNIL 77  
 40 KSKSLIRVENFEAFYFKQADNSGCPAEYEDLKLIGSLPKYALIELNNGKRRNNVNL 99  
 78 PYDATRYVLSNVDDPCSDYINASYIRGNFRREYITQGLPKGKDDPFMKVMEQNVN 137  
 100 PDISRYVLS-VQTHSTDYINANVMGHSKQPIATQGPLNTLKDFMVMVEKRVYA 158  
 138 IVMATQCEKGRKCDHWPPADQSLTYGDLLOMLSESVLPEWITREFKICGEBOLDH 197  
 159 IYMLTKCEGGRKCEYFSPSKQ-AQYGDITVANTSEVLPPEWITRDFVVMKMSSEH 217  
 198 RLIRHFHYTWPHGVPEFTQSLQFRTVRYNRSFGAPTVHCSAGVGRGTFFIAL 257  
 218 PL-RQPHFTSMPHGVPTDILLNFRYLVRYDMKQIPPEPILVHCSAGVGRGTFFIAL 276  
 258 DRILQQLDSKDSVDIYGAVHDLRLHRYVMVQTECOYVYLHQCVRDYLARK 308  
 277 DRLLYQLEINENTVDYGVLYDLRMHREPLMVQTEQYVFLNQCVLDIIRAK 327

DB 277 DRLLYQLEINENTVDYGVLYDLRMHREPLMVQTEQYVFLNQCVLDIIRAK 327

RESULT 11  
 062884\_RAT PRELIMINARY; PRT; 1216 AA.

AC 062884; RAT PRELIMINARY; PRT; 1216 AA.  
 DT 01-NOV-1996 (TRENBERG, 01, Last sequence update)  
 DT 01-NOV-1996 (TRENBERG, 01, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Vascular protein tyrosine phosphatase 1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NCBI\_Taxid=10116;  
 [1]  
 NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Miscar Kyoto; TISSUE=Aorta;  
 RX MEDLINE=96375109; PubMed=8781490;  
 RA Borges L.G., Seifert R.A., Grant F.J., Hart C.E., Distche C.M., Edelhoff S., Solica F.F., Lieberman M.A., Lindner V., Fischer E.H., Lok S., Bowen-Pope D.F.;  
 RA "Cloning and characterization of rat density-enhanced phosphatase-1, a protein tyrosine phosphatase expressed by vascular cells.";  
 RT Circ. Res. 79:570-580(1996).  
 RL -1- SUBCELLULAR LOCATION: Type I membrane protein (by similarity).  
 CC EMBL: U60790; AB53195.1; -; mRNA.  
 CC HSP: P18052; iPro.  
 CC RGD: 3454; RefSeq.  
 CC GO: GO:0016021; C: integral to membrane; IEA.  
 CC GO: GO:0016787; F: hydrolase activity; IEA.  
 CC GO: GO:0004725; F: protein tyrosine phosphatase activity; IEA.  
 CC GO: GO:0004872; F: receptor activity; IEA.  
 CC GO: GO:0004470; P: protein amino acid phosphorylation; IEA.  
 DR InterPro: IPR003961; FN III.  
 DR InterPro: IPR00387; TYR\_phosphatase.  
 DR InterPro: IPR00242; TYR\_PP.  
 DR Pfam: PF00041; fn3; 7.  
 DR Pfam: PF00102; Y\_phosphatase; 1.  
 DR PRINTS: PR00700; PRTPHPTASE.  
 DR SMART: SM00194; PTPC; 1.  
 DR PROSITE: PS00853; FN3; 8.  
 DR PROSITE: PS00853; TYR\_PHOSPHATASE\_1; 1.  
 DR PROSITE: PS00856; TYR\_PHOSPHATASE\_2; 1.  
 DR PROSITE: PS00855; TYR\_PHOSPHATASE\_PTP; 1.  
 DR Hydrolase; Repeat; Transmembrane.  
 SC SEQUENCE: 1216 AA; 134276 MW; 406139B10855391 CRC64;

Query Match 49.8%; Score 868.5; DB 2; Length 1216;  
 Best Local Similarity 55.7%; Pred. No. 6.4e-64;  
 Matches 162; Conservative 56; Mismatches 70; Indels 3; Gaps 3;

DB 18 KTSCEPIKINGEFGHFKMLQADSNVLSKEYEELKDVGRNOSCDIALPENNGKRRNNIL 77  
 40 KSKSLIRVENFEAFYFKQADNSGCPAEYEDLKLIGSLPKYALIELNNGKRRNNVNL 99  
 78 PYDATRYVLSNVDDPCSDYINASYIRGNFRREYITQGLPKGKDDPFMKVMEQNVN 137  
 100 PDISRYVLS-VQTHSTDYINANVMGHSKQPIATQGPLNTLKDFMVMVEKRVYA 158  
 138 IVMATQCEKGRKCDHWPPADQSLTYGDLLOMLSESVLPEWITREFKICGEBOLDH 197  
 159 IYMLTKCEGGRKCEYFSPSKQ-AQYGDITVANTSEVLPPEWITRDFVVMKMSSEH 217  
 198 RLIRHFHYTWPHGVPEFTQSLQFRTVRYNRSFGAPTVHCSAGVGRGTFFIAL 257  
 218 PL-RQPHFTSMPHGVPTDILLNFRYLVRYDMKQIPPEPILVHCSAGVGRGTFFIAL 276  
 258 DRILQQLDSKDSVDIYGAVHDLRLHRYVMVQTECOYVYLHQCVRDYLARK 308  
 277 DRLLYQLEINENTVDYGVLYDLRMHREPLMVQTEQYVFLNQCVLDIIRAK 327

DB 1132 DRLLYQLEINENTVDYGVLYDLRMHREPLMVQTEQYVFLNQCVLDIIRAK 1182

RESULT 12  
 PTPRJ MOUSE STANDARD; PRT; 1238 AA.

AC 064455;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Receptor-type tyrosine-protein phosphatase eta precursor (EC 3.1.3.48)  
 DE (Protein-tyrosine phosphatase eta) (R-PTP-eta) (HPTP beta-like tyrosine phosphatase) (Protein-tyrosine phosphatase receptor type J)  
 DE (Susceptibility to colon cancer-1).  
 GN Name=Ptprj; Synonyms=Byp, Soc1;  
 OS Mus musculus (Mouse)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_Taxid=10090;  
 [1]  
 NUCLEOTIDE SEQUENCE.  
 RC STRAIN=MBL-LPR/LPR;  
 RX MEDLINE=9610659; PubMed=8549806; DOI=10.1016/0014-5793(95)01415-2;  
 RA Kuzumochi S., Matsuda S., Matsuda Y., Salton T., Ohnogi M., Yamamoto T.;  
 RA "Molecular cloning and characterization of Byp, a murine receptor-type tyrosine phosphatase similar to human DEP-1.";  
 RT FEBS Lett. 378:7-14(1996).  
 RL -1- SUBCELLULAR LOCATION: Protein tyrosine phosphatase + H(2)O = protein tyrosine + phosphate.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- TISSUE SPECIFICITY: Expressed in every tissue examined.  
 CC -1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family. Receptor class 3 subfamily.  
 CC -1- SIMILARITY: Contains 8 fibronectin type-III domains.  
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 CC EMBL: D45212; BA08146.1; -; mRNA.  
 CC PIR: S68700; S68700.  
 CC HSP: P18052; iPro.  
 CC EMBL: ENSMUSG0000025314; Mus musculus.  
 DR MGI: MGI:104574; Ptpj.  
 DR GO: GO:0005615; C: extracellular space; TAS.  
 DR GO: GO:0016021; C: integral to membrane; TAS.



DR GO; GO:0007507, P:heart development; IMP.  
 DR GO; GO:0001570, P:vasculogenesis; IMP.  
 DR InterPro: IPR003361; FN III.  
 DR InterPro: IPR003387; TYR phosphatase.  
 DR InterPro: IPR002421; Tyr\_P.  
 DR Pfam: PF00041; fn3; 6.  
 DR Pfam: PF00102; X phosphatase; 1.  
 DR PRINTS: PR00700; PTPYPTPHASE.  
 DR SMART: SM00060; PTP; 7.  
 DR SMART: SM00184; PTP; 1.  
 DR PROSITE: PS00833; FN3; 1.  
 DR PROSITE: PS00833; TYR\_PHOSPHATASE\_1; 1.  
 DR PROSITE: PS00833; TYR\_PHOSPHATASE\_2; 1.  
 DR PROSITE: PS00833; TYR\_PHOSPHATASE\_PTP; 1.  
 KW Glycoprotein; Hydrolase; Protein phosphatase; Repeat; Signal;  
 KW Transmembrane.  
 FT SIGNAL 1 28  
 FT CHAIN 29 1238  
 FT TOPO\_DOM 29 876  
 FT TRANSMEM 877 897  
 FT TOPO\_DOM 898 1238  
 FT DOMAIN 40 130  
 FT DOMAIN 170 266  
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 FT DOMAIN 356 440  
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 FT DOMAIN 528 618  
 FT DOMAIN 620 712  
 FT DOMAIN 717 803  
 FT DOMAIN 942 1199  
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 FT CARBOHYD 538 538  
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 FT CARBOHYD 576 576  
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 FT CARBOHYD 691 691  
 FT CARBOHYD 725 725  
 FT CARBOHYD 811 811  
 FT CARBOHYD 838 838  
 SQ SEQUENCE 1238 AA; 136783 MW; 939479EDC8016835 CRC64;

Query Match 49.8%; Score 868.5; DB 1; Length 1238;

Best Local Similarity 55.7%; Pred. No. 6.5e-64;  
 Matches 162; Conservative 56; Mismatches 70; Indels 3; Gaps 3;  
 QY 18 KTSCPIKINQFEGHFMKLQADSNVILSKYEELKDVGNOSCDIALPENRGRNRYNNIL 77  
 DB 917 KKSLLIRVENFEAFYFKQADSNVILSKYEELKDVGNOSCDIALPENRGRNRYNNIL 976  
 QY 78 PYDARVTLNVDDPCSDYINASYIPGNFRREYIVTQGLPQTRDQDFWKVWQVNHV 137  
 DB 977 PYDISRVTLKSVQHSKCDYINASYIPGNFRREYIVTQGLPQTRDQDFWKVWQVNHV 1035  
 QY 138 IWTATQCVKRWKCHVHPADODSLYGLLIQMLSESVLPKWTREPFVIGCEQDLAH 197  
 DB 1036 IWTATQCVKRWKCHVHPADODSLYGLLIQMLSESVLPKWTREPFVIGCEQDLAH 1094  
 QY 198 RLIRPHRYTWPDPGVPTTQSLIQFRTVRYDYNRSPEAGPTVHCAGVGTGTFIAL 257  
 DB 1095 PLRQHPFTSPDGVPTTQSLIQFRTVRYDYNRSPEAGPTVHCAGVGTGTFIAL 1153  
 QY 258 DRILQDLQSDKSDVYIGAVHDLRLRVMVQTECYVYLHOCVADVLRLAK 308  
 DB 1154 DRILQDLQSDKSDVYIGAVHDLRLRVMVQTECYVYLHOCVADVLRLAK 1204  
 RESULT 13  
 ID 0541R5 MOUSE PRELIMINARY; PRT; 1238 AA.  
 AC 0541R5  
 DT 13-SEP-2005 (TrEMBLrel 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel 31, Last annotation update).  
 DE PPRK.  
 GN Name=Peprj;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN (1)  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=BL6/C;  
 RA van Wezel T., Rulvenkamp C.A.T., Zanon C., Staessen A.P.M., Vlcek C.,  
 RA Csikos T., Tripodis N., Groot P.C., Dauwerse H., van Ommen G.J.B.,  
 RA Dement P.;  
 RT "Positional cloning identifies Peprj as the candidate for colon cancer  
 RT susceptibility QTL Sccl.";  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).  
 DR EMBL: AY038891; AAK36030.1; -; mRNA.  
 DR MGI: MGI:104574; Peprj.  
 DR GO; GO:0005615; C:extracellular space; TAS.  
 DR GO; GO:0016021; C:integral to membrane; TAS.  
 DR GO; GO:0007507; P:heart development; IMP.  
 DR GO; GO:0001570; P:vasculogenesis; IMP.  
 KW Hydrolase; Repeat; Transmembrane.  
 SQ SEQUENCE 1238 AA; 136782 MW; 939479EDC8016835 CRC64;  
 Query Match 49.8%; Score 868.5; DB 2; Length 1238;  
 Best Local Similarity 55.7%; Pred. No. 6.5e-64;  
 Matches 162; Conservative 56; Mismatches 70; Indels 3; Gaps 3;  
 QY 18 KTSCPIKINQFEGHFMKLQADSNVILSKYEELKDVGNOSCDIALPENRGRNRYNNIL 77  
 DB 917 KKSLLIRVENFEAFYFKQADSNVILSKYEELKDVGNOSCDIALPENRGRNRYNNIL 976  
 QY 78 PYDARVTLNVDDPCSDYINASYIPGNFRREYIVTQGLPQTRDQDFWKVWQVNHV 137  
 DB 977 PYDISRVTLKSVQHSKCDYINASYIPGNFRREYIVTQGLPQTRDQDFWKVWQVNHV 1035  
 QY 138 IWTATQCVKRWKCHVHPADODSLYGLLIQMLSESVLPKWTREPFVIGCEQDLAH 197  
 DB 1036 IWTATQCVKRWKCHVHPADODSLYGLLIQMLSESVLPKWTREPFVIGCEQDLAH 1094



RA Shue B.C., Siden-Klamas I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spieding A.C., Stapleton M., Strong R., Sun E.,  
 RA Strydom R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Williams S.M., Wesserman D.A., Weisbeck G.M., Weisbach J.,  
 RA Williams S.M., Woodage T., Moley K.C., Mu D., Yang S., Yao Q.A.,  
 RA Ye J., Yen R.-P., Zaveri J.S., Zhan W., Zhang G., Zhao Q., Zheng U.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
 RA "The genome sequence of *Drosophila melanogaster*,"  
 RA Science 287:2185-2195(2000).  
 RT  
 RL [4]  
 RP GENOME REANNOTATION AND ALTERNATIVE SPLICING.  
 RP MEDLINE=22426069; PubMed=1253572;  
 RA Maira S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
 RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochuk S.E.,  
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
 RA Bertecourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,  
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,  
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
 RA Lewis S.E.,  
 RA "Annotation of the *Drosophila melanogaster* euchromatic genome: a  
 RT systematic review,"  
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).  
 RP [5]  
 RP NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA) (ISOFORM LONG).  
 RP STRAIN=Berkeley; TISSUE=Embryo.  
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.W.,  
 RA Champagne M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,  
 RA George R.A., Gonzalez M., Guatin H., Krommiller B., Li P.W., Liao G.,  
 RA Miranda A., Mungall C.J., Nunco J., Paclob J.M., Parasg V., Park S.,  
 RA Patel S., Phouanavong S., Wan K.H., Yu C., Lewis S.E., Rubin G.M.,  
 RA Celniker S.E.,  
 RA Submitted (Feb-2003) to the EMBL/GenBank/DBJ databases.  
 RL  
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein  
 CC tyrosine + phosphate.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=4;  
 CC Name=Long;  
 CC IsoId=P35992-1; Sequence=Displayed;  
 CC Name=Short;  
 CC IsoId=P35992-2; Sequence=VSP\_005143, VSP\_005144;  
 CC Name=A; Synonyms=B;  
 CC IsoId=P35992-3; Sequence=VSP\_015266;  
 CC Note=No experimental confirmation available;  
 CC Name=C;  
 CC IsoId=P35992-4; Sequence=VSP\_015264, VSP\_015265;  
 CC Note=No experimental confirmation available;  
 CC -1- TISSUE SPECIFICITY: Selectively expressed in anterior commissure  
 CC and its junctions with the longitudinal tracts.  
 CC -1- SIMILARITY: Belongs to the tyrosine-phosphatase family.  
 CC Receptor class subfamily.  
 CC -1- SIMILARITY: Contains 1 tyrosine-protein phosphatase domain.  
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC  
 CC EMBL: M80465; AAA28484.1; -; mRNA.  
 CC EMBL: M80538; AAA28952.1; -; mRNA.  
 CC EMBL: AE003486; AAF48072.2; -; Genomic DNA.  
 CC EMBL: AE003486; AAF48072.2; -; Genomic DNA.  
 CC EMBL: BT004474; AAC042638.1; -; mRNA.  
 CC PIR: D41214; D41214.  
 CC HSSP: P10566; 11AB.  
 CC TrEMBL: C05817; Drosophila melanogaster.  
 CC FlyBase: FBgn0004370, FlyPID.  
 CC GO: 0004725; P:protein tyrosine phosphatase activity; IDA.  
 CC GO: 0004470; P:protein amino acid dephosphorylation; IDA.  
 CC InterPro: IPR000282; CytoC\_receptor\_2.

DR InterPro: IPR003961; FN III.  
 DR InterPro: IPR003962; FN III subd.  
 DR InterPro: IPR003967; Tyr\_Pp.  
 DR InterPro: IPR000242; Tyr\_Pp.  
 DR Pfam: PF00441; fn3; 10.  
 DR Pfam: PF0102; X\_phosphatase; 1.  
 DR PRINTS: PR00014; PNTYPRIT.  
 DR PRINTS: PR00700; PRTYPRITASE.  
 DR SMART: SM00060; FN3; 11.  
 DR SMART: SM00194; PTPC; 1.  
 DR PROSITE: PS50853; FN3; 11.  
 DR PROSITE: PS00383; TYR\_PHOSPHATASE\_1; 1.  
 DR PROSITE: PS50056; TYR\_PHOSPHATASE\_PTP; 1.  
 DR PROSITE: PS50055; TYR\_PHOSPHATASE\_PTP; 1.  
 KW Alternative splicing; Glycoprotein; Hydrolase; Protein phosphatase;  
 KW Repeat; Signal; Transmembrane.  
 FT SIGNAL 1 42  
 FT CHAIN 1 1631  
 FT TOPO DOM 43 1197  
 FT TOPO DOM 1198 1218  
 FT TRANS MEM 1219 1631  
 FT TOPO DOM 43 119  
 FT DOMAIN 120 214  
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 FT DOMAIN 403 493  
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 FT DOMAIN 862 955  
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 Blast Local Similarity 55.6%; Pred. No. 3; 1-62;  
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 QY 22 PIKIQEGHFMCLQDSDNYLISKEYEELKQVGNOSCDLALPENRKNRYNNIIPYA 81  
 DB 1251 PILIKNFARHRLMSHSDPFRSBEELKAVGRQCFCTADLPCKRKNRKFNIIPYH 1310

Qy 82 TRVGLSNVDDDDPCSDYINASYYIPGNFRREYIVTGGPLBGTXODPEWKNVWBOVNIWV 141  
Db 1311 SHFKLOPVDDDESDYINANNVPGHNSPREFIVTGGPLHSTRDDPFWRMCWESNSRAIVWL 1370  
Qy 142 TQCEKGRVWCDHVPAPADSLIYGDLIOMLSESVLPENTIREKIC-GEOLDARLI 200  
Db 1371 TRCEKGRERKCDQYWNDFVPEFYGDIKVQILNDSHTADWMTFMDLRSBQ---RIL 1426  
Qy 201 RHFNVTWPDHGVPETTQSLIQFRTVRYINRSPGAGPTVHCSAGYGTGTFLADRI 260  
Db 1427 RHFNFTWPDHGVPEPPQTLVRFVRAFRDRIGAB--ORPIVHCSAGVGRSGTFTLDR 1484  
Qy 261 LQOLDSKDSVDIYGAVHDLRLHRVHWVQTECOYVYLHQCVRDYLARK 308  
Db 1485 LQOINTSDYDIFGIYAMRKERVWVQTEOOYICIHQCLLAVLEGE 1532

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Job time : 233 secs